



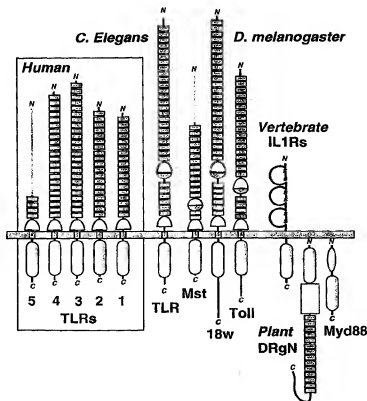
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(54) Title: HUMAN TOLL-LIKE RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS

## (57) Abstract

Nucleic acids encoding nine human receptors, designated DNAX Toll-like receptors 2-10 (DTRL2-10), homologous to the Drosophila Toll receptor and the human IL-1 receptor, purified DTLR proteins and fragments thereof, mono-/polyclonal antibodies against these receptors, and methods for diagnostic and therapeutic use.



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### HUMAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

This filing claims priority from U.S. Patent  
5 Applications USSN 60/044,293, filed May 7, 1997; USSN  
60/072,212, filed January 22, 1998; and USSN 60/076,947,  
filed March 5, 1998, each of which is incorporated herein  
by reference.

### FIELD OF THE INVENTION

The present invention relates to compositions and  
methods for affecting mammalian physiology, including  
morphogenesis or immune system function. In particular,  
it provides nucleic acids, proteins, and antibodies which  
15 regulate development and/or the immune system.  
Diagnostic and therapeutic uses of these materials are  
also disclosed.

### BACKGROUND OF THE INVENTION

20 Recombinant DNA technology refers generally to  
techniques of integrating genetic information from a  
donor source into vectors for subsequent processing, such  
as through introduction into a host, whereby the  
transferred genetic information is copied and/or  
25 expressed in the new environment. Commonly, the genetic  
information exists in the form of complementary DNA  
(cDNA) derived from messenger RNA (mRNA) coding for a  
desired protein product. The carrier is frequently a  
plasmid having the capacity to incorporate cDNA for later  
30 replication in a host and, in some cases, actually to  
control expression of the cDNA and thereby direct  
synthesis of the encoded product in the host.

For some time, it has been known that the mammalian  
immune response is based on a series of complex cellular  
35 interactions, called the "immune network". Recent  
research has provided new insights into the inner  
workings of this network. While it remains clear that

much of the immune response does, in fact, revolve around the network-like interactions of lymphocytes, macrophages, granulocytes, and other cells, immunologists now generally hold the opinion that soluble proteins, known as lymphokines, cytokines, or monokines, play critical roles in controlling these cellular interactions. Thus, there is considerable interest in the isolation, characterization, and mechanisms of action of cell modulatory factors, an understanding of which will lead to significant advancements in the diagnosis and therapy of numerous medical abnormalities, e.g., immune system disorders.

Lymphokines apparently mediate cellular activities in a variety of ways. They have been shown to support the proliferation, growth, and/or differentiation of pluripotential hematopoietic stem cells into vast numbers of progenitors comprising diverse cellular lineages which make up a complex immune system. Proper and balanced interactions between the cellular components are necessary for a healthy immune response. The different cellular lineages often respond in a different manner when lymphokines are administered in conjunction with other agents.

Cell lineages especially important to the immune response include two classes of lymphocytes: B-cells, which can produce and secrete immunoglobulins (proteins with the capability of recognizing and binding to foreign matter to effect its removal), and T-cells of various subsets that secrete lymphokines and induce or suppress the B-cells and various other cells (including other T-cells) making up the immune network. These lymphocytes interact with many other cell types.

Another important cell lineage is the mast cell (which has not been positively identified in all mammalian species), which is a granule-containing connective tissue cell located proximal to capillaries throughout the body. These cells are found in especially

high concentrations in the lungs, skin, and gastrointestinal and genitourinary tracts. Mast cells play a central role in allergy-related disorders, particularly anaphylaxis as follows: when selected  
5 antigens crosslink one class of immunoglobulins bound to receptors on the mast cell surface, the mast cell degranulates and releases mediators, e.g., histamine, serotonin, heparin, and prostaglandins, which cause allergic reactions, e.g., anaphylaxis.

10 Research to better understand and treat various immune disorders has been hampered by the general inability to maintain cells of the immune system in vitro. Immunologists have discovered that culturing many of these cells can be accomplished through the use of T-  
15 cell and other cell supernatants, which contain various growth factors, including many of the lymphokines.

The interleukin-1 family of proteins includes the IL-1 $\alpha$ , the IL-1 $\beta$ , the IL-1RA, and recently the IL-1 $\gamma$  (also designated Interferon-Gamma Inducing Factor, IGIF).  
20 This related family of genes have been implicated in a broad range of biological functions. See Dinarello (1994) FASEB J. 8:1314-1325; Dinarello (1991) Blood 77:1627-1652; and Okamura, et al. (1995) Nature 378:88-91.

25 In addition, various growth and regulatory factors exist which modulate morphogenetic development. This includes, e.g., the Toll ligands, which signal through binding to receptors which share structural, and mechanistic, features characteristic of the IL-1  
30 receptors. See, e.g., Lemaitre, et al. (1996) Cell 86:973-983; and Belvin and Anderson (1996) Ann. Rev. Cell & Devel. Biol. 12:393-416.

From the foregoing, it is evident that the discovery and development of new soluble proteins and their  
35 receptors, including ones similar to lymphokines, should contribute to new therapies for a wide range of degenerative or abnormal conditions which directly or

indirectly involve development, differentiation, or function, e.g., of the immune system and/or hematopoietic cells. In particular, the discovery and understanding of novel receptors for lymphokine-like molecules which enhance or potentiate the beneficial activities of other lymphokines would be highly advantageous. The present invention provides new receptors for ligands exhibiting similarity to interleukin-1 like compositions and related compounds, and methods for their use.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a schematic comparison of the protein architectures of Drosophila and human DTLRs, and their relationship to vertebrate IL-1 receptors and plant disease resistance proteins. Three Drosophila (Dm) DTLRs (Toll, 18w, and the Mst ORF fragment) (Morisato and Anderson (1995) Ann. Rev. Genet. 29:371-399; Chiang and Beachy (1994) Mech. Develop. 47:225-239; Mitcham, et al. (1996) J. Biol. Chem. 271:5777-5783; and Eldon, et al. (1994) Develop. 120:885-899) are arrayed beside four complete (DTLRs 1-4) and one partial (DTLR5) human (Hu) receptors. Individual LRRs in the receptor ectodomains that are flagged by PRINTS (Attwood, et al. (1997) Nucleic Acids Res. 25:212-217) are explicitly noted by boxes; 'top' and 'bottom' Cys-rich clusters that flank the C- or N-terminal ends of LRR arrays are respectively drawn by apposed half-circles. The loss of the internal Cys-rich region in DTLRs 1-5 largely accounts for their smaller ectodomains (558, 570, 690, and 652 aa, respectively) when compared to the 784 and 977 aa extensions of Toll and 18w. The incomplete chains of DmMst and HuDTLR5 (519 and 153 aa ectodomains, respectively) are represented by dashed lines. The intracellular signaling module common to DTLRs, IL-1-type receptors (IL-1Rs), the intracellular protein Myd88, and the tobacco disease resistance gene N product (DRGN) is indicated below the membrane. See, e.g., Hardiman, et

al. (1996) Oncogene 13:2467-2475; and Rock, et al. (1998) Proc. Nat'l Acad. Sci. USA 95:588-. Additional domains include the trio of Ig-like modules in IL-1Rs (disulfide-linked loops); the DRGN protein features an NTPase domain (box) and Myd88 has a death domain (black oval).

Figures 2A-2B show conserved structural patterns in the signaling domains of Toll- and IL-1-like cytokine receptors, and two divergent modular proteins. Figure 2A shows a sequence alignment of the common TH domain.

DTLRs are labeled as in Figure 1; the human (Hu) or mouse (Mo) IL-1 family receptors (IL-1R1-6) are sequentially numbered as earlier proposed (Hardiman, et al. (1996) Oncogene 13:2467-2475); Myd88 and the sequences from tobacco (To) and flax, *L. usitatissimum* (Lu), represent C- and N-terminal domains, respectively, of larger, multidomain molecules. Ungapped blocks of sequence (numbered 1-10) are boxed. Triangles indicate deleterious mutations, while truncations N-terminal of the arrow eliminate bioactivity in human IL-1R1 (Heguy, et al. (1992) J. Biol. Chem. 267:2605-2609). PHD (Rost and Sander (1994) Proteins 19:55-72) and DSC (King and Sternberg (1996) Protein Sci. 5:2298-2310) secondary structure predictions of  $\alpha$ -helix (H),  $\beta$ -strand (E), or coil (L) are marked. The amino acid shading scheme depicts chemically similar residues: hydrophobic, acidic, basic, Cys, aromatic, structure-breaking, and tiny. Diagnostic sequence patterns for IL-1Rs, DTLRs, and full alignment (ALL) were derived by Consensus at a stringency of 75%. Symbols for amino acid subsets are (see internet site for detail): o, alcohol; l, aliphatic; ., any amino acid; a, aromatic; c, charged; h, hydrophobic; -, negative; p, polar; +, positive; s, small; u, tiny; t, turnlike. Figure 2B shows a topology diagram of the proposed TH  $\beta/\alpha$  domain fold. The parallel  $\beta$ -sheet (with  $\beta$ -strands A-E as yellow triangles) is seen at its C-terminal end;  $\alpha$ -helices (circles labeled 1-5) link the  $\beta$ -strands; chain connections are to the front (visible) or

back (hidden). Conserved, charged residues at the C-end of the  $\beta$ -sheet are noted in gray (Asp) or as a lone black (Arg) residue (see text).

Figure 3 shows evolution of a signaling domain superfamily. The multiple TH module alignment of Figure 2A was used to derive a phylogenetic tree by the Neighbor-Joining method (Thompson, et al. (1994) Nucleic Acids Res. 22:4673-4680). Proteins labeled as in the alignment; the tree was rendered with TreeView.

Figures 4A-4D show FISH chromosomal mapping of human DTLR genes. Denatured chromosomes from synchronous cultures of human lymphocytes were hybridized to biotinylated DTLR cDNA probes for localization. The assignment of the FISH mapping data (left, Figures 4A, DTLR2; 4B, DTLR3; 4C, DTLR4; 4D, DTLR5) with chromosomal bands was achieved by superimposing FISH signals with DAPI banded chromosomes (center panels). Heng and Tsui (1994) Meth. Molec. Biol. 33:109-122. Analyses are summarized in the form of human chromosome ideograms (right panels).

Figures 5A-5F show mRNA blot analyses of Human DTLRs. Human multiple tissue blots (He, heart; Br, brain; Pl, placenta; Lu, lung; Li, liver; Mu, muscle; Ki, kidney; Pn, Pancreas; Sp, spleen; Th, thymus; Pr, prostate; Te, testis; Ov, ovary, SI, small intestine; Co, colon; PBL, peripheral blood lymphocytes) and cancer cell line (promyelocytic leukemia, HL60; cervical cancer, HELAS3; chronic myelogenous leukemia, K562; lymphoblastic leukemia, Molt4; colorectal adenocarcinoma, SW480; melanoma, G361; Burkitt's Lymphoma Raji, Burkitt's; colorectal adenocarcinoma, SW480; lung carcinoma, A549) containing approximately 2  $\mu$ g of poly(A)<sup>+</sup> RNA per lane were probed with radiolabeled cDNAs encoding DTLR1 (Figures 5A-5C), DTLR2 (Figure 5D), DTLR3 (Figure 5E), and DTLR4 (Figure 5F) as described. Blots were exposed to X-ray film for 2 days (Figures 5A-5C) or one week (Figure 5D-5F) at -70° C with intensifying screens. An



anomalous 0.3 kB species appears in some lanes;  
hybridization experiments exclude a message encoding a  
DTLR cytoplasmic fragment.

#### SUMMARY OF THE INVENTION

5       The present invention is directed to nine novel  
related mammalian receptors, e.g., human, Toll receptor  
like molecular structures, designated DTLR2, DTLR3,  
DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9, and DTLR10, and  
their biological activities. It includes nucleic acids  
10 coding for the polypeptides themselves and methods for  
their production and use. The nucleic acids of the  
invention are characterized, in part, by their homology  
to cloned complementary DNA (cDNA) sequences enclosed  
herein.

15       In certain embodiments, the invention provides a  
composition of matter selected from the group of: a  
substantially pure or recombinant DTLR2 protein or  
peptide exhibiting at least about 85% sequence identity  
over a length of at least about 12 amino acids to SEQ ID  
20 NO: 4; a natural sequence DTLR2 of SEQ ID NO: 4; a fusion  
protein comprising DTLR2 sequence; a substantially pure  
or recombinant DTLR3 protein or peptide exhibiting at  
least about 85% sequence identity over a length of at  
least about 12 amino acids to SEQ ID NO: 6; a natural  
25 sequence DTLR3 of SEQ ID NO: 6; a fusion protein  
comprising DTLR3 sequence; a substantially pure or  
recombinant DTLR4 protein or peptide exhibiting at least  
about 85% sequence identity over a length of at least  
about 12 amino acids to SEQ ID NO: 26; a natural sequence  
30 DTLR4 of SEQ ID NO: 26; a fusion protein comprising DTLR4  
sequence; a substantially pure or recombinant DTLR5  
protein or peptide exhibiting at least about 85% sequence  
identity over a length of at least about 12 amino acids  
to SEQ ID NO: 10; a natural sequence DTLR5 of SEQ ID NO:  
35 10; and a fusion protein comprising DTLR5 sequence.

In other embodiments, the invention provides a  
composition of matter selected from the group of: a

substantially pure or recombinant DTLR6 protein or peptide exhibiting at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 12; a natural sequence DTLR6 of SEQ ID NO: 12; a fusion protein comprising DTLR6 sequence; a substantially pure or recombinant DTLR7 protein or peptide exhibiting at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 16 or 18 or; a natural sequence DTLR7 of SEQ ID NO: 16 or 18; a fusion protein comprising DTLR7 sequence; a substantially pure or recombinant DTLR8 protein or peptide exhibiting at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 32; a natural sequence DTLR8 of SEQ ID NO: 32; a fusion protein comprising DTLR8 sequence; a substantially pure or recombinant DTLR9 protein or peptide exhibiting at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 22; a natural sequence DTLR9 of SEQ ID NO: 22; and a fusion protein comprising DTLR9 sequence; a substantially pure or recombinant DTLR10 protein or peptide exhibiting at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 34; a natural sequence DTLR10 of SEQ ID NO: 34; and a fusion protein comprising DTLR10 sequence.

Preferably, the substantially pure or isolated protein comprises a segment exhibiting sequence identity to a corresponding portion of a DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR 7, DTLR8, DTLR9, or DTLR10, wherein: the homology is at least about 90% identity and the portion is at least about 9 amino acids; the homology is at least about 80% identity and the portion is at least about 17 amino acids; or the homology is at least about 70% identity and the portion is at least about 25 amino acids. In specific embodiments, the composition of matter: is DTLR2, which comprises a mature sequence of SEQ ID NO: 4; or exhibits a post-translational+

modification pattern distinct from natural DTLR2; is DTLR3, which comprises a mature sequence of SEQ ID NO: 6; or exhibits a post-translational modification pattern distinct from natural DTLR3; is DTLR4, which: comprises a  
5 mature sequence of SEQ ID NO: 26; or exhibits a post-translational modification pattern distinct from natural DTLR4; or is DTLR5, which: comprises the complete sequence of SEQ ID NO: 10; or exhibits a post-translational modification pattern distinct from natural  
10 DTLR5; or is DTLR6, which comprises a mature sequence of SEQ ID NO: 12; or exhibits a post-translational modification pattern distinct from natural DTLR6; is DTLR7, which comprises a mature sequence of SEQ ID NO: 16 or 18; or exhibits a post-translational modification  
15 pattern distinct from natural DTLR7; is DTLR8, which: comprises a mature sequence of SEQ ID NO: 32; or exhibits a post-translational modification pattern distinct from natural DTLR8; or is DTLR9, which: comprises the complete sequence of SEQ ID NO: 22; or exhibits a post-translational modification pattern distinct from natural  
20 DTLR9; or is DTLR10, which: comprises the complete sequence of SEQ ID NO: 34; or exhibits a post-translational modification pattern distinct from natural DTLR10; or the composition of matter may be a protein or  
25 peptide which: is from a warm blooded animal selected from a mammal, including a primate, such as a human; comprises at least one polypeptide segment of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34; exhibits a plurality of portions exhibiting said identity; is a  
30 natural allelic variant of DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9, or DTLR10; has a length at least about 30 amino acids; exhibits at least two non-overlapping epitopes which are specific for a primate  
DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9,  
35 or DTLR10; exhibits a sequence identity at least about 90% over a length of at least about 20 amino acids to a primate DTLR2, DTLR3, DTLR4, DTLR5, DTLR6; exhibits at

least two non-overlapping epitopes which are specific for a primate DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9, or DTLR10; exhibits a sequence identity at least about 90% over a length of at least about 20 amino acids to a primate DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9, or DTLR10; is glycosylated; has a molecular weight of at least 100 kD with natural glycosylation; is a synthetic polypeptide; is attached to a solid substrate; is conjugated to another chemical moiety; is a 5-fold or less substitution from natural sequence; or is a deletion or insertion variant from a natural sequence.

Other embodiments include a composition comprising: a sterile DTLR2 protein or peptide; or the DTLR2 protein or peptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration; a sterile DTLR3 protein or peptide; or the DTLR3 protein or peptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration; a sterile DTLR4 protein or peptide; or the DTLR4 protein or peptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration; a sterile DTLR5 protein or peptide; or the DTLR5 protein or peptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration; a sterile DTLR6 protein or peptide; or the DTLR6 protein or peptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration; a sterile DTLR7 protein or peptide; or the DTLR7 protein or peptide and a carrier,

wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration; a sterile DTLR8 protein or peptide; or the DTLR8 protein or peptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration; a sterile DTLR9 protein or peptide; or the DTLR9 protein or peptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration; a sterile DTLR10 protein or peptide; or the DTLR10 protein or peptide and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration.

In certain fusion protein embodiments, the invention provides a fusion protein comprising: mature protein sequence of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34; a detection or purification tag, including a FLAG, His6, or Ig sequence; or sequence of another receptor protein.

Various kit embodiments include a kit comprising a DTLR protein or polypeptide, and: a compartment comprising the protein or polypeptide; and/or instructions for use or disposal of reagents in the kit.

Binding compound embodiments include those comprising an antigen binding site from an antibody, which specifically binds to a natural DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9, or DTLR10 protein, wherein: the protein is a primate protein; the binding compound is an Fv, Fab, or Fab2 fragment; the binding compound is conjugated to another chemical moiety; or the antibody: is raised against a peptide sequence of a mature polypeptide of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34; is raised against a mature

DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9 or DTLR10; is raised to a purified human DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9 or DTLR10; is immunoselected; is a polyclonal antibody; binds to a

5 denatured DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9 or DTLR10; exhibits a  $K_d$  to antigen of at least 30  $\mu\text{M}$ ; is attached to a solid substrate, including a bead or plastic membrane; is in a sterile composition; or is detectably labeled, including a radioactive or

10 fluorescent label. A binding composition kit often comprises the binding compound, and: a compartment comprising said binding compound; and/or instructions for use or disposal of reagents in the kit. Often the kit is capable of making a qualitative or quantitative analysis.

15 Other compositions include a composition comprising: a sterile binding compound, or the binding compound and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral

20 administration.

Nucleic acid embodiments include an isolated or recombinant nucleic acid encoding a DTLR2-10 protein or peptide or fusion protein, wherein: the DTLR is from a mammal; or the nucleic acid: encodes an antigenic peptide

25 sequence of of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34; encodes a plurality of antigenic peptide sequences of of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34; exhibits at least about 80% identity to a natural cDNA encoding said segment; is an expression

30 vector; further comprises an origin of replication; is from a natural source; comprises a detectable label; comprises synthetic nucleotide sequence; is less than 6 kb, preferably less than 3 kb; is from a mammal, including a primate; comprises a natural full length

35 coding sequence; is a hybridization probe for a gene encoding said DTLR; or is a PCR primer, PCR product, or mutagenesis primer. A cell, tissue, or organ comprising

such a recombinant nucleic acid is also provided. Preferably, the cell is: a prokaryotic cell; a eukaryotic cell; a bacterial cell; a yeast cell; an insect cell; a mammalian cell; a mouse cell; a primate cell; or a human cell. Kits are provided comprising such nucleic acids, and: a compartment comprising said nucleic acid; a compartment further comprising a primate DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9 or DTLR10 protein or polypeptide; and/or instructions for use or disposal of reagents in the kit. Often, the kit is capable of making a qualitative or quantitative analysis.

Other embodiments include a nucleic acid which: hybridizes under wash conditions of 30° C and less than 2M salt to SEQ ID NO: 3; hybridizes under wash conditions of 30° C and less than 2 M salt to SEQ ID NO: 5; hybridizes under wash conditions of 30° C and less than 2M salt to SEQ ID NO: 25; hybridizes under wash conditions of 30° C and less than 2 M salt to SEQ ID NO: 9; hybridizes under wash conditions of 30° C and less than 2M salt to SEQ ID NO: 11; hybridizes under wash conditions of 30° C and less than 2 M salt to SEQ ID NO: 15 or 17; hybridizes under wash conditions of 30° C and less than 2M salt to SEQ ID NO: 31; hybridizes under wash conditions of 30° C and less than 2 M salt to SEQ ID NO: 21; hybridizes under wash conditions of 30° C and less than 2 M salt to SEQ ID NO: 33; exhibits at least about 85% identity over a stretch of at least about 30 nucleotides to a primate DTLR2 DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9 or DTLR10.

Preferably, such nucleic acid will have such properties, wherein: wash conditions are at 45° C and/or 500 mM salt; or the identity is at least 90% and/or the stretch is at least 55 nucleotides. More preferably, the wash conditions are at 55° C and/or 150 mM salt; or the identity is at least 95% and/or the stretch is at least 75 nucleotides.

The invention also provides a method of modulating physiology or development of a cell or tissue culture cells comprising contacting the cell with an agonist or antagonist of a mammalian DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9, or DTLR10.

#### DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

##### I. General

The present invention provides the amino acid sequence and DNA sequence of mammalian, herein primate DNAX Toll like receptor molecules (DTLR) having particular defined properties, both structural and biological. These have been designated herein as DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9, and DTLR10, respectively, and increase the number of members of the human Toll like receptor family from 1 to 10. Various cDNAs encoding these molecules were obtained from primate, e.g., human, cDNA sequence libraries. Other primate or other mammalian counterparts would also be desired.

Some of the standard methods applicable are described or referenced, e.g., in Maniatis, et al. (1982) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor Press; Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual, (2d ed.), vols 1-3, CSH Press, NY; Ausubel, et al., Biology, Greene Publishing Associates, Brooklyn, NY; or Ausubel, et al. (1987 and periodic supplements) Current Protocols in Molecular Biology, Greene/Wiley, New York; each of which is incorporated herein by reference.

A complete nucleotide and corresponding amino acid sequence of a human DTLR1 coding segment is shown in SEQ ID NO: 1 and 2. See also Nomura, et al. (1994) DNA Res 1:27-35. A complete nucleotide and corresponding amino acid sequence of a human DTLR2 coding segment is shown in SEQ ID NO: 3 and 4. A complete nucleotide and



corresponding amino acid sequence of a human DTLR3 coding segment is shown in SEQ ID NO: 5 and 6. A complete nucleotide and corresponding amino acid sequence of a human DTLR4 coding segment is shown in SEQ ID NO: 7 and 8. An alternate nucleic acid and corresponding amino acid sequence of a human DTLR4 coding segment is provided in SEQ ID NO: 25 and 26. A partial nucleotide and corresponding amino acid sequence of a human DTLR5 coding segment is shown in SEQ ID NO: 9 and 10. A complete nucleotide and corresponding amino acid sequence of a human DTLR6 coding segment is shown in SEQ ID NO: 11 and 12 and a partial sequence of a mouse DTLR6 is provided in SEQ ID NO: 13 and 14. Additional mouse DTLR6 sequence is provided in SEQ ID NO: 27 and 29 (nucleotide sequence) and SEQ ID NO: 28 and 30 (amino acid sequence). Partial nucleotide (SEQ ID NO: 15 and 17) and corresponding amino acid sequence (SEQ ID NO: 16 and 18) of a human DTLR7 coding segment is also provided. Partial nucleotide and corresponding amino acid sequence of a human DTLR8 coding segment is shown in SEQ ID NO: 19 and 20. A more complete nucleotide and corresponding amino acid sequence of a human DTLR coding segment is shown in SEQ ID NO: 31 and 32. Partial nucleotide and corresponding amino acid sequence of a human DTLR9 coding segment is shown in SEQ ID NO: 21 and 22. Partial nucleotide and corresponding amino acid sequence of a human DTLR10 coding segment is shown in SEQ ID NO: 23 and 24. More complete nucleotide and corresponding amino acid sequence of a human DTLR10 coding segment is shown in SEQ ID NO: 33 and 34. A partial nucleotide sequence for a mouse DTLR10 coding segment is provided in SEQ ID NO: 35.

Table 1: Comparison of intracellular domains of human DTLRs.  
 DTLR1 is SEQ ID NO: 2; DTLR2 is SEQ ID NO: 4; DTLR3 is SEQ ID NO: 6; DTLR4 is SEQ ID NO: 8; DTLR5 is SEQ ID NO: 10; and DTLR6 is SEQ ID NO: 12. Particularly important and conserved, e.g., characteristic, residues correspond, across the DTLRs, to SEQ ID NO: 18 residues tyr10-tyr13; trp26; cys46; trp52; pro54-gly55; ser69; lys71; trp134-pro135; and phe144-trp145.

5	DTLR1	QRNLQFHAFISYSGHD---SFVWKNE LLPNLEKEG----MQICLHERNF
10	DTLR9	KENLQFHAFISYSYEH---SAWVKSELVPYLEKED----IQICLHERNF
	DTLR8	-----NELIPNLEKEDGS---ILICLYESYF
	DTLR2	SRNICYDAFVYSYERD---AYWVENLMVQLENFNFP---FKLC LHKRDF
	DTLR6	SPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREK---HFNLCLEERDW
	DTLR7	TSQTFYDAVISYDTKDASVTDVWVNLRYHLEESRDK---NVLLCLEERDW
15	DTLR10	EDALPYDAFVVFDTKXSAVADVYNELRGQLEECRGRW-ALRLCLEERDW
	DTLR4	RGENIYDAFVIYSSQD---EDWVRNELVKNLEEGVPP---FQLCLHYRDF
	DTLR5	PMYKYDAYLCFSSKD---FTWVQNALLKHLDTQYSDQNRFNLCFEERDF
	DTLR3	TEQFEYAAAYIIHAYKD---KDWVWEHFSSMEKEDQS---LKFCLEERDF
20		: . . : * : :
	DTLR1	VPGKSIVENIITC-IEKSYKSI FVLSPNFVQSEWCH-YELYFAHNNLFHE
	DTLR9	VPGKSIVENI INC-IEKSYKSI FVLSPNFVQSEWCH-YELYFAHNNLFHE
	DTLR8	DPGKSISENIVSF-IEKSYKSI FVLSPNFVQSEWCH-YEYFAHNNLFHE
	DTLR2	IPGKIWDNIIDS-IEKSHKT VFLSEN FVKSEWCK-YELDFSHFLRFE
25	DTLR6	LPGQPVLENLSQS-IQLSKKT VFMVMDKYAKTENFK-IAFYLSHQR L MDE
	DTLR7	DPLGLAIIDNLMQS-INQSKKT VFLTKYAKSNWFK-TAFYLXLQRLMGE
	DTLR10	LPGKTLFENLWAS-VYGSRKTLFVLATDRVSGLLR-AIFLLAQORLLE-
	DTLR4	IPGVAIAANI IHEGFHKS R KVI VVVSQHFIQSRWCI-FEYFIAQTWQFLS
	DTLR5	VPGENRIANIQDA-IWNSRKIVCLVSRHFLRDGWCL-EAFSYAQGRCLSD
30	DTLR3	EAGVFELEAIVNS-IKRSRKII FVITHLLKDLPLCKRKFVHVAVQQAIEQ
		. * : . * * : : : :
	DTLR1	GSNSLILILLEPI PQYSIPSSYHKLKSLMARRTYLEWPKEKSKRGLFWAN
35	DTLR9	GSNNLILILLEPI PQNSIPNKYHKLKALMTQRTYLQWPKEKSKRGLFWAN
	DTLR8	NSDHI LILILLEPI PFYCIPTRYHKLKALLEKKAYLEWPKDRRRCGLFWAN
	DTLR2	NNDAAI LILILLEPI EKKAIPORFCKLRKIMNTKTYLEWPMDEAOREGFWVN
	DTLR6	KVDV IILIFLEKPFQK---SKFLQLRKLRCGSSVLEWPTNFQAH P YFWQC
	DTLR7	NMDV IIFILLEPVLQH---SPYLR LRQRICKSS I LQWPDNPKAERLFWQT
	DTLR10	
40	DTLR4	SRAGI I FIVLQKVEKT-LLRQQVELYRLLSRNTYLEWEDSVLGRHIFWRH
	DTLR5	LNSALIMVVGSLSQY-QLMKHQSIRGFVQKQQYLRWPEDLQDVGWFLHK
	DTLR3	NLDSIILVLEBIPDYKLNHALCLRRGMFKSHCILNWVPVKRERIGAFPHK
45	DTLR1	LRAAINIKLTQAKK-----
	DTLR9	-----
	DTLR8	LRAAVNVNVLATREMYELQTFELNEESRGSTISLMRTDCL
	DTLR2	LRAAIKS-----
	DTLR6	LKNA LATDNHVAYSQVFKETV-----
50	DTLR7	LXNVVLTENDSRYNMNVDSIKQY-----
	DTLR10	-----
	DTLR4	LRKALLDGKSWNPGTVGTGNWQEATSI-----
	DTLR5	LSQQILKEKEKEKKDNNIPLQTVATIS-----
	DTLR3	LQVALGSKNSVH-----
55		

As used herein, the term DNAX Toll like receptor 2 (DTLR2) shall be used to describe a protein comprising a protein or peptide segment having or sharing the amino acid sequence shown in SEQ ID NO: 4, or a substantial fragment thereof. Similarly, with a DTLR3 and SEQ ID NO: 6; DTLR4 and SEQ ID NO: 26; DTLR5 and SEQ ID NO: 10; DTLR6 and SEQ ID NO: 12; DTLR7 and SEQ ID NO: 16 and 18; DTLR8 and SEQ ID NO: 32; DTLR9 and SEQ ID NO: 22; and DTLR10 and SEQ ID NO: 34.

The invention also includes a protein variations of the respective DTLR allele whose sequence is provided, e.g., a mutein agonist or antagonist. Typically, such agonists or antagonists will exhibit less than about 10% sequence differences, and thus will often have between 1- and 11-fold substitutions, e.g., 2-, 3-, 5-, 7-fold, and others. It also encompasses allelic and other variants, e.g., natural polymorphic, of the protein described. Typically, it will bind to its corresponding biological receptor with high affinity, e.g., at least about 100 nM, usually better than about 30 nM, preferably better than about 10 nM, and more preferably at better than about 3 nM. The term shall also be used herein to refer to related naturally occurring forms, e.g., alleles, polymorphic variants, and metabolic variants of the mammalian protein.

This invention also encompasses proteins or peptides having substantial amino acid sequence identity with the amino acid sequence in SEQ ID NO: 4. It will include sequence variants with relatively few substitutions, e.g., preferably less than about 3-5. Similar features apply to the other DTLR sequences provided in SEQ ID NO: 6, 26, 10, 12, 16, 18, 32, 22 and 34.

A substantial polypeptide "fragment", or "segment", is a stretch of amino acid residues of at least about 8 amino acids, generally at least 10 amino acids, more generally at least 12 amino acids, often at least 14

amino acids, more often at least 16 amino acids, typically at least 18 amino acids, more typically at least 20 amino acids, usually at least 22 amino acids, more usually at least 24 amino acids, preferably at least 26 amino acids, more preferably at least 28 amino acids, and, in particularly preferred embodiments, at least about 30 or more amino acids. Sequences of segments of different proteins can be compared to one another over appropriate length stretches.

Amino acid sequence homology, or sequence identity, is determined by optimizing residue matches, if necessary, by introducing gaps as required. See, e.g., Needleham, et al., (1970) J. Mol. Biol. 48:443-453; Sankoff, et al., (1983) chapter one in Time Warps, String Edits, and Macromolecules: The Theory and Practice of Sequence Comparison, Addison-Wesley, Reading, MA; and software packages from IntelliGenetics, Mountain View, CA; and the University of Wisconsin Genetics Computer Group (GCG), Madison, WI; each of which is incorporated herein by reference. This changes when considering conservative substitutions as matches. Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Homologous amino acid sequences are intended to include natural allelic and interspecies variations in the cytokine sequence. Typical homologous proteins or peptides will have from 50-100% homology (if gaps can be introduced), to 60-100% homology (if conservative substitutions are included) with an amino acid sequence segment of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34. Homology measures will be at least about 70%, generally at least 76%, more generally at least 81%, often at least 85%, more often at least 88%, typically at least 90%, more typically at least 92%, usually at least 94%, more usually at least 95%,

preferably at least 96%, and more preferably at least 97%, and in particularly preferred embodiments, at least 98% or more. The degree of homology will vary with the length of the compared segments. Homologous proteins or peptides, such as the allelic variants, will share most biological activities with the embodiments described in SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34. Particularly interesting regions of comparison, at the amino acid or nucleotide levels, correspond to those within each of the blocks 1-10, or intrablock regions, corresponding to those indicated in Figure 2A.

As used herein, the term "biological activity" is used to describe, without limitation, effects on inflammatory responses, innate immunity, and/or morphogenic development by respective ligands. For example, these receptors should, like IL-1 receptors, mediate phosphatase or phosphorylase activities, which activities are easily measured by standard procedures. See, e.g., Hardie, et al. (eds. 1995) The Protein Kinase FactBook vols. I and II, Academic Press, San Diego, CA; Hanks, et al. (1991) Meth. Enzymol. 200:38-62; Hunter, et al. (1992) Cell 70:375-388; Lewin (1990) Cell 61:743-752; Pines, et al. (1991) Cold Spring Harbor Symp. Quant. Biol. 56:449-463; and Parker, et al. (1993) Nature 363:736-738. The receptors exhibit biological activities much like regulatable enzymes, regulated by ligand binding. However, the enzyme turnover number is more close to an enzyme than a receptor complex. Moreover, the numbers of occupied receptors necessary to induce such enzymatic activity is less than most receptor systems, and may number closer to dozens per cell, in contrast to most receptors which will trigger at numbers in the thousands per cell. The receptors, or portions thereof, may be useful as phosphate labeling enzymes to label general or specific substrates.

The terms ligand, agonist, antagonist, and analog of, e.g., a DTLR, include molecules that modulate the

characteristic cellular responses to Toll ligand like proteins, as well as molecules possessing the more standard structural binding competition features of ligand-receptor interactions, e.g., where the receptor is a natural receptor or an antibody. The cellular responses likely are mediated through binding of various Toll ligands to cellular receptors related to, but possibly distinct from, the type I or type II IL-1 receptors. See, e.g., Belvin and Anderson (1996) Ann. Rev. Cell Dev. Biol. 12:393-416; Morisato and Anderson (1995) Ann. Rev. Genetics 29:371-3991 and Hultmark (1994) Nature 367:116-117.

Also, a ligand is a molecule which serves either as a natural ligand to which said receptor, or an analog thereof, binds, or a molecule which is a functional analog of the natural ligand. The functional analog may be a ligand with structural modifications, or may be a wholly unrelated molecule which has a molecular shape which interacts with the appropriate ligand binding determinants. The ligands may serve as agonists or antagonists, see, e.g., Goodman, et al. (eds) (1990) Goodman & Gilman's: The Pharmacological Bases of Therapeutics, Pergamon Press, New York.

Rational drug design may also be based upon structural studies of the molecular shapes of a receptor or antibody and other effectors or ligands. Effectors may be other proteins which mediate other functions in response to ligand binding, or other proteins which normally interact with the receptor. One means for determining which sites interact with specific other proteins is a physical structure determination, e.g., x-ray crystallography or 2 dimensional NMR techniques. These will provide guidance as to which amino acid residues form molecular contact regions. For a detailed description of protein structural determination, see, e.g., Blundell and Johnson (1976) Protein

Crystallography, Academic Press, New York, which is hereby incorporated herein by reference.

## II. Activities

5       The Toll like receptor proteins will have a number of different biological activities, e.g., in phosphate metabolism, being added to or removed from specific substrates, typically proteins. Such will generally result in modulation of an inflammatory function, other  
10 innate immunity response, or a morphological effect. The DTLR2, 3, 4, 5, 6, 7, 8, 9, or 10 proteins are homologous to other Toll like receptor proteins, but each have structural differences. For example, a human DTLR2 gene coding sequence probably has about 70% identity with the  
15 nucleotide coding sequence of mouse DTLR2. At the amino acid level, there is also likely to be reasonable identity.

      The biological activities of the DTLRs will be related to addition or removal of phosphate moieties to  
20 substrates, typically in a specific manner, but occasionally in a non specific manner. Substrates may be identified, or conditions for enzymatic activity may be assayed by standard methods, e.g., as described in Hardie, et al. (eds. 1995) The Protein Kinase FactBook  
25 vols. I and II, Academic Press, San Diego, CA; Hanks, et al. (1991) Meth. Enzymol. 200:38-62; Hunter, et al. (1992) Cell 70:375-388; Lewin (1990) Cell 61:743-752; Pines, et al. (1991) Cold Spring Harbor Symp. Quant. Biol. 56:449-463; and Parker, et al. (1993) Nature  
30 363:736-738.

## III. Nucleic Acids

      This invention contemplates use of isolated nucleic acid or fragments, e.g., which encode these or closely  
35 related proteins, or fragments thereof, e.g., to encode a corresponding polypeptide, preferably one which is biologically active. In addition, this invention covers

isolated or recombinant DNA which encodes such proteins or polypeptides having characteristic sequences of the respective DTLRs, individually or as a group. Typically, the nucleic acid is capable of hybridizing, under  
5 appropriate conditions, with a nucleic acid sequence segment shown in SEQ ID NOs: 3, 5, 25, 9, 11, 15, 17, 31, 21, or 33, but preferably not with a corresponding segment of SEQ ID NO: 1. Said biologically active protein or polypeptide can be a full length protein, or  
10 fragment, and will typically have a segment of amino acid sequence highly homologous to one shown in SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34. Further, this invention covers the use of isolated or recombinant nucleic acid, or fragments thereof, which encode proteins  
15 having fragments which are equivalent to the DTLR2-10 proteins. The isolated nucleic acids can have the respective regulatory sequences in the 5' and 3' flanks, e.g., promoters, enhancers, poly-A addition signals, and others from the natural gene.

20 An "isolated" nucleic acid is a nucleic acid, e.g., an RNA, DNA, or a mixed polymer, which is substantially pure, e.g., separated from other components which naturally accompany a native sequence, such as ribosomes, polymerases, and flanking genomic sequences from the  
25 originating species. The term embraces a nucleic acid sequence which has been removed from its naturally occurring environment, and includes recombinant or cloned DNA isolates, which are thereby distinguishable from naturally occurring compositions, and chemically  
30 synthesized analogs or analogs biologically synthesized by heterologous systems. A substantially pure molecule includes isolated forms of the molecule, either completely or substantially pure.

An isolated nucleic acid will generally be a  
35 homogeneous composition of molecules, but will, in some embodiments, contain heterogeneity, preferably minor. This heterogeneity is typically found at the polymer ends



or portions not critical to a desired biological function or activity.

A "recombinant" nucleic acid is typically defined either by its method of production or its structure. In  
5 reference to its method of production, e.g., a product made by a process, the process is use of recombinant nucleic acid techniques, e.g., involving human intervention in the nucleotide sequence. Typically this intervention involves in vitro manipulation, although  
10 under certain circumstances it may involve more classical animal breeding techniques. Alternatively, it can be a nucleic acid made by generating a sequence comprising fusion of two fragments which are not naturally contiguous to each other, but is meant to exclude  
15 products of nature, e.g., naturally occurring mutants as found in their natural state. Thus, for example, products made by transforming cells with any unnaturally occurring vector is encompassed, as are nucleic acids comprising sequence derived using any synthetic  
20 oligonucleotide process. Such a process is often done to replace a codon with a redundant codon encoding the same or a conservative amino acid, while typically introducing or removing a restriction enzyme sequence recognition site. Alternatively, the process is performed to join  
25 together nucleic acid segments of desired functions to generate a single genetic entity comprising a desired combination of functions not found in the commonly available natural forms, e.g., encoding a fusion protein. Restriction enzyme recognition sites are often the target  
30 of such artificial manipulations, but other site specific targets, e.g., promoters, DNA replication sites, regulation sequences, control sequences, or other useful features may be incorporated by design. A similar concept is intended for a recombinant, e.g., fusion,  
35 polypeptide. This will include a dimeric repeat. Specifically included are synthetic nucleic acids which, by genetic code redundancy, encode equivalent

polypeptides to fragments of DTLR2-10 and fusions of sequences from various different related molecules, e.g., other IL-1 receptor family members.

A "fragment" in a nucleic acid context is a  
5 contiguous segment of at least about 17 nucleotides, generally at least 21 nucleotides, more generally at least 25 nucleotides, ordinarily at least 30 nucleotides, more ordinarily at least 35 nucleotides, often at least 39 nucleotides, more often at least 45 nucleotides,  
10 typically at least 50 nucleotides, more typically at least 55 nucleotides, usually at least 60 nucleotides, more usually at least 66 nucleotides, preferably at least 72 nucleotides, more preferably at least 79 nucleotides, and in particularly preferred embodiments will be at  
15 least 85 or more nucleotides. Typically, fragments of different genetic sequences can be compared to one another over appropriate length stretches, particularly defined segments such as the domains described below.

A nucleic acid which codes for a DTLR2-10 will be  
20 particularly useful to identify genes, mRNA, and cDNA species which code for itself or closely related proteins, as well as DNAs which code for polymorphic, allelic, or other genetic variants, e.g., from different individuals or related species. Preferred probes for  
25 such screens are those regions of the interleukin which are conserved between different polymorphic variants or which contain nucleotides which lack specificity, and will preferably be full length or nearly so. In other situations, polymorphic variant specific sequences will  
30 be more useful.

This invention further covers recombinant nucleic acid molecules and fragments having a nucleic acid sequence identical to or highly homologous to the isolated DNA set forth herein. In particular, the  
35 sequences will often be operably linked to DNA segments which control transcription, translation, and DNA

replication. These additional segments typically assist in expression of the desired nucleic acid segment.

Homologous, or highly identical, nucleic acid sequences, when compared to one another or the sequences shown in SEQ ID NO: 3, 5, 25, 9, 11, 15, 17, 31, 21, or 33 exhibit significant similarity. The standards for homology in nucleic acids are either measures for homology generally used in the art by sequence comparison or based upon hybridization conditions. Comparative hybridization conditions are described in greater detail below.

Substantial identity in the nucleic acid sequence comparison context means either that the segments, or their complementary strands, when compared, are identical when optimally aligned, with appropriate nucleotide insertions or deletions, in at least about 60% of the nucleotides, generally at least 66%, ordinarily at least 71%, often at least 76%, more often at least 80%, usually at least 84%, more usually at least 88%, typically at least 91%, more typically at least about 93%, preferably at least about 95%, more preferably at least about 96 to 98% or more, and in particular embodiments, as high at about 99% or more of the nucleotides, including, e.g., segments encoding structural domains such as the segments described below. Alternatively, substantial identity will exist when the segments will hybridize under selective hybridization conditions, to a strand or its complement, typically using a sequence derived from SEQ ID NO: 3, 5, 25, 9, 11, 15, 17, 31, 21, or 33. Typically, selective hybridization will occur when there is at least about 55% homology over a stretch of at least about 14 nucleotides, more typically at least about 65%, preferably at least about 75%, and more preferably at least about 90%. See, Kanehisa (1984) Nuc. Acids Res. 12:203-213, which is incorporated herein by reference. The length of homology comparison, as described, may be over longer stretches, and in certain embodiments will be

over a stretch of at least about 17 nucleotides, generally at least about 20 nucleotides, ordinarily at least about 24 nucleotides, usually at least about 28 nucleotides, typically at least about 32 nucleotides, more typically at least about 40 nucleotides, preferably at least about 50 nucleotides, and more preferably at least about 75 to 100 or more nucleotides.

Stringent conditions, in referring to homology in the hybridization context, will be stringent combined conditions of salt, temperature, organic solvents, and other parameters typically controlled in hybridization reactions. Stringent temperature conditions will usually include temperatures in excess of about 30° C, more usually in excess of about 37° C, typically in excess of about 45° C, more typically in excess of about 55° C, preferably in excess of about 65° C, and more preferably in excess of about 70° C. Stringent salt conditions will ordinarily be less than about 500 mM, usually less than about 400 mM, more usually less than about 300 mM, typically less than about 200 mM, preferably less than about 100 mM, and more preferably less than about 80 mM, even down to less than about 20 mM. However, the combination of parameters is much more important than the measure of any single parameter. See, e.g., Wetmur and Davidson (1968) J. Mol. Biol. 31:349-370, which is hereby incorporated herein by reference.

Alternatively, for sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optical alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (see generally Ausubel et al., supra).

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a tree or dendrogram showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng and Doolittle (1987) J. Mol. Evol. 35:351-360. The method used is similar to the method described by Higgins and Sharp (1989) CABIOS 5:151-153. The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. For example, a reference sequence can be compared to other test sequences to determine the percent sequence identity relationship using the following

parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps.

Another example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described Altschul, et al. (1990) J. Mol. Biol. 215:403-410. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a wordlength (W) of 11, the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci.

USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ( $P(N)$ ), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

A further indication that two nucleic acid sequences of polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions, as described below.

The isolated DNA can be readily modified by nucleotide substitutions, nucleotide deletions, nucleotide insertions, and inversions of nucleotide stretches. These modifications result in novel DNA sequences which encode this protein or its derivatives. These modified sequences can be used to produce mutant proteins (muteins) or to enhance the expression of variant species. Enhanced expression may involve gene amplification, increased transcription, increased translation, and other mechanisms. Such mutant DTLR-like derivatives include predetermined or site-specific mutations of the protein or its fragments, including silent mutations using genetic code degeneracy. "Mutant DTLR" as used herein encompasses a polypeptide otherwise falling within the homology definition of the DTLR as set

forth above, but having an amino acid sequence which differs from that of other DTLR-like proteins as found in nature, whether by way of deletion, substitution, or insertion. In particular, "site specific mutant DTLR" encompasses a protein having substantial homology with a protein of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34, and typically shares most of the biological activities or effects of the forms disclosed herein.

Although site specific mutation sites are predetermined, mutants need not be site specific. Mammalian DTLR mutagenesis can be achieved by making amino acid insertions or deletions in the gene, coupled with expression. Substitutions, deletions, insertions, or any combinations may be generated to arrive at a final construct. Insertions include amino- or carboxy-terminal fusions. Random mutagenesis can be conducted at a target codon and the expressed mammalian DTLR mutants can then be screened for the desired activity. Methods for making substitution mutations at predetermined sites in DNA having a known sequence are well known in the art, e.g., by M13 primer mutagenesis. See also Sambrook, et al. (1989) and Ausubel, et al. (1987 and periodic Supplements).

The mutations in the DNA normally should not place coding sequences out of reading frames and preferably will not create complementary regions that could hybridize to produce secondary mRNA structure such as loops or hairpins.

The phosphoramidite method described by Beaucage and Carruthers (1981) Tetra. Letts. 22:1859-1862, will produce suitable synthetic DNA fragments. A double stranded fragment will often be obtained either by synthesizing the complementary strand and annealing the strand together under appropriate conditions or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.



Polymerase chain reaction (PCR) techniques can often be applied in mutagenesis. Alternatively, mutagenesis primers are commonly used methods for generating defined mutations at predetermined sites. See, e.g., Innis, et al. (eds. 1990) PCR Protocols: A Guide to Methods and Applications Academic Press, San Diego, CA; and Dieffenbach and Dveksler (1995; eds.) PCR Primer: A Laboratory Manual Cold Spring Harbor Press, CSH, NY.

#### 10 IV. Proteins, Peptides

As described above, the present invention encompasses primate DTLR2-10, e.g., whose sequences are disclosed in SEQ ID NOS: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34, and described above. Allelic and other variants are also contemplated, including, e.g., fusion proteins combining portions of such sequences with others, including epitope tags and functional domains.

The present invention also provides recombinant proteins, e.g., heterologous fusion proteins using segments from these rodent proteins. A heterologous fusion protein is a fusion of proteins or segments which are naturally not normally fused in the same manner. Thus, the fusion product of a DTLR with an IL-1 receptor is a continuous protein molecule having sequences fused in a typical peptide linkage, typically made as a single translation product and exhibiting properties, e.g., sequence or antigenicity, derived from each source peptide. A similar concept applies to heterologous nucleic acid sequences.

In addition, new constructs may be made from combining similar functional or structural domains from other related proteins, e.g., IL-1 receptors or other DTLRs, including species variants. For example, ligand-binding or other segments may be "swapped" between different new fusion polypeptides or fragments. See, e.g., Cunningham, et al. (1989) Science 243:1330-1336; and O'Dowd, et al. (1988) J. Biol. Chem. 263:15985-15992,

each of which is incorporated herein by reference. Thus, new chimeric polypeptides exhibiting new combinations of specificities will result from the functional linkage of receptor-binding specificities. For example, the ligand binding domains from other related receptor molecules may be added or substituted for other domains of this or related proteins. The resulting protein will often have hybrid function and properties. For example, a fusion protein may include a targetting domain which may serve to provide sequestering of the fusion protein to a particular subcellular organelle.

Candidate fusion partners and sequences can be selected from various sequence data bases, e.g., GenBank, c/o IntelliGenetics, Mountain View, CA; and BCG, University of Wisconsin Biotechnology Computing Group, Madison, WI, which are each incorporated herein by reference.

The present invention particularly provides muteins which bind Toll ligands, and/or which are affected in signal transduction. Structural alignment of human DTLR1-10 with other members of the IL-1 family show conserved features/residues. See, e.g., Figure 3A. Alignment of the human DTLR sequences with other members of the IL-1 family indicates various structural and functionally shared features. See also, Bazan, et al. (1996) Nature 379:591; Lodi, et al. (1994) Science 263:1762-1766; Sayle and Milner-White (1995) TIBS 20:374-376; and Gronenberg, et al. (1991) Protein Engineering 4:263-269.

The IL-1 $\alpha$  and IL-1 $\beta$  ligands bind an IL-1 receptor type I as the primary receptor and this complex then forms a high affinity receptor complex with the IL-1 receptor type III. Such receptor subunits are probably shared with the new IL-1 family members.

Similar variations in other species counterparts of DTLR2-10 sequences, e.g., in the corresponding regions, should provide similar interactions with ligand or

substrate. Substitutions with either mouse sequences or human sequences are particularly preferred. Conversely, conservative substitutions away from the ligand binding interaction regions will probably preserve most signaling activities.

"Derivatives" of the primate DTLR2-10 include amino acid sequence mutants, glycosylation variants, metabolic derivatives and covalent or aggregative conjugates with other chemical moieties. Covalent derivatives can be prepared by linkage of functionalities to groups which are found in the DTLR amino acid side chains or at the N- or C- termini, e.g., by means which are well known in the art. These derivatives can include, without limitation, aliphatic esters or amides of the carboxyl terminus, or of residues containing carboxyl side chains, O-acyl derivatives of hydroxyl group-containing residues, and N-acyl derivatives of the amino terminal amino acid or amino-group containing residues, e.g., lysine or arginine. Acyl groups are selected from the group of alkyl-moieties including C3 to C18 normal alkyl, thereby forming alkanoyl aroyl species.

In particular, glycosylation alterations are included, e.g., made by modifying the glycosylation patterns of a polypeptide during its synthesis and processing, or in further processing steps. Particularly preferred means for accomplishing this are by exposing the polypeptide to glycosylating enzymes derived from cells which normally provide such processing, e.g., mammalian glycosylation enzymes. Deglycosylation enzymes are also contemplated. Also embraced are versions of the same primary amino acid sequence which have other minor modifications, including phosphorylated amino acid residues, e.g., phosphotyrosine, phosphoserine, or phosphothreonine.

A major group of derivatives are covalent conjugates of the receptors or fragments thereof with other proteins or polypeptides. These derivatives can be synthesized in

recombinant culture such as N- or C-terminal fusions or by the use of agents known in the art for their usefulness in cross-linking proteins through reactive side groups. Preferred derivatization sites with cross-linking agents are at free amino groups, carbohydrate moieties, and cysteine residues.

Fusion polypeptides between the receptors and other homologous or heterologous proteins are also provided. Homologous polypeptides may be fusions between different receptors, resulting in, for instance, a hybrid protein exhibiting binding specificity for multiple different Toll ligands, or a receptor which may have broadened or weakened specificity of substrate effect. Likewise, heterologous fusions may be constructed which would exhibit a combination of properties or activities of the derivative proteins. Typical examples are fusions of a reporter polypeptide, e.g., luciferase, with a segment or domain of a receptor, e.g., a ligand-binding segment, so that the presence or location of a desired ligand may be easily determined. See, e.g., Dull, et al., U.S. Patent No. 4,859,609, which is hereby incorporated herein by reference. Other gene fusion partners include glutathione-S-transferase (GST), bacterial  $\beta$ -galactosidase, trpE, Protein A,  $\beta$ -lactamase, alpha amylase, alcohol dehydrogenase, and yeast alpha mating factor. See, e.g., Godowski, et al. (1988) Science 241:812-816.

The phosphoramidite method described by Beaucage and Carruthers (1981) Tetra. Letts. 22:1859-1862, will produce suitable synthetic DNA fragments. A double stranded fragment will often be obtained either by synthesizing the complementary strand and annealing the strand together under appropriate conditions or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

Such polypeptides may also have amino acid residues which have been chemically modified by phosphorylation,

sulfonation, biotinylation, or the addition or removal of other moieties, particularly those which have molecular shapes similar to phosphate groups. In some embodiments, the modifications will be useful labeling reagents, or  
5 serve as purification targets, e.g., affinity ligands.

Fusion proteins will typically be made by either recombinant nucleic acid methods or by synthetic polypeptide methods. Techniques for nucleic acid manipulation and expression are described generally, for  
10 example, in Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed.), Vols. 1-3, Cold Spring Harbor Laboratory, and Ausubel, et al. (eds. 1987 and periodic supplements) Current Protocols in Molecular Biology,  
Greene/Wiley, New York, which are each incorporated  
15 herein by reference. Techniques for synthesis of polypeptides are described, for example, in Merrifield (1963) J. Amer. Chem. Soc. 85:2149-2156; Merrifield (1986) Science 232: 341-347; and Atherton, et al. (1989) Solid Phase Peptide Synthesis: A Practical Approach, IRL  
20 Press, Oxford; each of which is incorporated herein by reference. See also Dawson, et al. (1994) Science 266:776-779 for methods to make larger polypeptides.

This invention also contemplates the use of derivatives of a DTLR2-10 other than variations in amino  
25 acid sequence or glycosylation. Such derivatives may involve covalent or aggregative association with chemical moieties. These derivatives generally fall into three classes: (1) salts, (2) side chain and terminal residue covalent modifications, and (3) adsorption complexes, for  
30 example with cell membranes. Such covalent or aggregative derivatives are useful as immunogens, as reagents in immunoassays, or in purification methods such as for affinity purification of a receptor or other  
binding molecule, e.g., an antibody. For example, a Toll  
35 ligand can be immobilized by covalent bonding to a solid support such as cyanogen bromide-activated Sepharose, by methods which are well known in the art, or adsorbed onto

polyolefin surfaces, with or without glutaraldehyde cross-linking, for use in the assay or purification of a DTLR receptor, antibodies, or other similar molecules. The ligand can also be labeled with a detectable group, for example radioiodinated by the chloramine T procedure, covalently bound to rare earth chelates, or conjugated to another fluorescent moiety for use in diagnostic assays.

A DTLR of this invention can be used as an immunogen for the production of antisera or antibodies specific, e.g., capable of distinguishing between other IL-1 receptor family members, for the DTLR or various fragments thereof. The purified DTLR can be used to screen monoclonal antibodies or antigen-binding fragments prepared by immunization with various forms of impure preparations containing the protein. In particular, the term "antibodies" also encompasses antigen binding fragments of natural antibodies, e.g., Fab, Fab2, Fv, etc. The purified DTLR can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous receptor. Additionally, DTLR fragments may also serve as immunogens to produce the antibodies of the present invention, as described immediately below. For example, this invention contemplates antibodies having binding affinity to or being raised against the amino acid sequences shown in SEQ ID NOS: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34, fragments thereof, or various homologous peptides. In particular, this invention contemplates antibodies having binding affinity to, or having been raised against, specific fragments which are predicted to be, or actually are, exposed at the exterior protein surface of the native DTLR.

The blocking of physiological response to the receptor ligands may result from the inhibition of binding of the ligand to the receptor, likely through competitive inhibition. Thus, in vitro assays of the

present invention will often use antibodies or antigen binding segments of these antibodies, or fragments attached to solid phase substrates. These assays will also allow for the diagnostic determination of the effects of either ligand binding region mutations and modifications, or other mutations and modifications, e.g., which affect signaling or enzymatic function.

This invention also contemplates the use of competitive drug screening assays, e.g., where neutralizing antibodies to the receptor or fragments compete with a test compound for binding to a ligand or other antibody. In this manner, the neutralizing antibodies or fragments can be used to detect the presence of a polypeptide which shares one or more binding sites to a receptor and can also be used to occupy binding sites on a receptor that might otherwise bind a ligand.

#### V. Making Nucleic Acids and Protein

DNA which encodes the protein or fragments thereof can be obtained by chemical synthesis, screening cDNA libraries, or by screening genomic libraries prepared from a wide variety of cell lines or tissue samples. Natural sequences can be isolated using standard methods and the sequences provided herein. Other species counterparts can be identified by hybridization techniques, or by various PCR techniques, combined with or by searching in sequence databases, e.g., GenBank.

This DNA can be expressed in a wide variety of host cells for the synthesis of a full-length receptor or fragments which can in turn, for example, be used to generate polyclonal or monoclonal antibodies; for binding studies; for construction and expression of modified ligand binding or kinase/phosphatase domains; and for structure/function studies. Variants or fragments can be expressed in host cells that are transformed or transfected with appropriate expression vectors. These

molecules can be substantially free of protein or cellular contaminants, other than those derived from the recombinant host, and therefore are particularly useful in pharmaceutical compositions when combined with a pharmaceutically acceptable carrier and/or diluent. The protein, or portions thereof, may be expressed as fusions with other proteins.

Expression vectors are typically self-replicating DNA or RNA constructs containing the desired receptor gene or its fragments, usually operably linked to suitable genetic control elements that are recognized in a suitable host cell. These control elements are capable of effecting expression within a suitable host. The specific type of control elements necessary to effect expression will depend upon the eventual host cell used. Generally, the genetic control elements can include a prokaryotic promoter system or a eukaryotic promoter expression control system, and typically include a transcriptional promoter, an optional operator to control the onset of transcription, transcription enhancers to elevate the level of mRNA expression, a sequence that encodes a suitable ribosome binding site, and sequences that terminate transcription and translation. Expression vectors also usually contain an origin of replication that allows the vector to replicate independently of the host cell.

The vectors of this invention include those which contain DNA which encodes a protein, as described, or a fragment thereof encoding a biologically active equivalent polypeptide. The DNA can be under the control of a viral promoter and can encode a selection marker. This invention further contemplates use of such expression vectors which are capable of expressing eukaryotic cDNA coding for such a protein in a prokaryotic or eukaryotic host, where the vector is compatible with the host and where the eukaryotic cDNA coding for the receptor is inserted into the vector such



that growth of the host containing the vector expresses the cDNA in question. Usually, expression vectors are designed for stable replication in their host cells or for amplification to greatly increase the total number of copies of the desirable gene per cell. It is not always necessary to require that an expression vector replicate in a host cell, e.g., it is possible to effect transient expression of the protein or its fragments in various hosts using vectors that do not contain a replication origin that is recognized by the host cell. It is also possible to use vectors that cause integration of the protein encoding portion or its fragments into the host DNA by recombination.

Vectors, as used herein, comprise plasmids, viruses, bacteriophage, integratable DNA fragments, and other vehicles which enable the integration of DNA fragments into the genome of the host. Expression vectors are specialized vectors which contain genetic control elements that effect expression of operably linked genes. Plasmids are the most commonly used form of vector but all other forms of vectors which serve an equivalent function and which are, or become, known in the art are suitable for use herein. See, e.g., Pouwels, et al. (1985 and Supplements) Cloning Vectors: A Laboratory Manual, Elsevier, N.Y., and Rodriquez, et al. (eds) Vectors: A Survey of Molecular Cloning Vectors and Their Uses, Butterworth, Boston, 1988, which are incorporated herein by reference.

Transformed cells are cells, preferably mammalian, that have been transformed or transfected with receptor vectors constructed using recombinant DNA techniques. Transformed host cells usually express the desired protein or its fragments, but for purposes of cloning, amplifying, and manipulating its DNA, do not need to express the subject protein. This invention further contemplates culturing transformed cells in a nutrient medium, thus permitting the receptor to accumulate in the

cell membrane. The protein can be recovered, either from the culture or, in certain instances, from the culture medium.

For purposes of this invention, nucleic sequences  
5 are operably linked when they are functionally related to each other. For example, DNA for a presequence or secretory leader is operably linked to a polypeptide if it is expressed as a preprotein or participates in directing the polypeptide to the cell membrane or in  
10 secretion of the polypeptide. A promoter is operably linked to a coding sequence if it controls the transcription of the polypeptide; a ribosome binding site is operably linked to a coding sequence if it is positioned to permit translation. Usually, operably  
15 linked means contiguous and in reading frame, however, certain genetic elements such as repressor genes are not contiguously linked but still bind to operator sequences that in turn control expression.

Suitable host cells include prokaryotes, lower  
20 eukaryotes, and higher eukaryotes. Prokaryotes include both gram negative and gram positive organisms, e.g., E. coli and B. subtilis. Lower eukaryotes include yeasts, e.g., S. cerevisiae and Pichia, and species of the genus Dictyostelium. Higher eukaryotes include established  
25 tissue culture cell lines from animal cells, both of non-mammalian origin, e.g., insect cells, and birds, and of mammalian origin, e.g., human, primates, and rodents.

Prokaryotic host-vector systems include a wide variety of vectors for many different species. As used  
30 herein, E. coli and its vectors will be used generically to include equivalent vectors used in other prokaryotes. A representative vector for amplifying DNA is pBR322 or many of its derivatives. Vectors that can be used to express the receptor or its fragments include, but are  
35 not limited to, such vectors as those containing the lac promoter (pUC-series); trp promoter (pBR322-trp); Ipp promoter (the pIN-series); lambda-pP or pR promoters

(pOTS); or hybrid promoters such as ptac (pDR540). See Brosius, et al. (1988) "Expression Vectors Employing Lambda-, trp-, lac-, and Ipp-derived Promoters", in Vectors: A Survey of Molecular Cloning Vectors and Their  
5 Uses, (eds. Rodriguez and Denhardt), Butterworth, Boston, Chapter 10, pp. 205-236, which is incorporated herein by reference.

Lower eukaryotes, e.g., yeasts and Dictyostelium, may be transformed with DTLR sequence containing vectors.

10 For purposes of this invention, the most common lower eukaryotic host is the baker's yeast, Saccharomyces cerevisiae. It will be used to generically represent lower eukaryotes although a number of other strains and species are also available. Yeast vectors typically  
15 consist of a replication origin (unless of the integrating type), a selection gene, a promoter, DNA encoding the receptor or its fragments, and sequences for translation termination, polyadenylation, and transcription termination. Suitable expression vectors  
20 for yeast include such constitutive promoters as 3-phosphoglycerate kinase and various other glycolytic enzyme gene promoters or such inducible promoters as the alcohol dehydrogenase 2 promoter or metallothioneine promoter. Suitable vectors include derivatives of the  
25 following types: self-replicating low copy number (such as the YRp-series), self-replicating high copy number (such as the YEp-series); integrating types (such as the YIp-series), or mini-chromosomes (such as the YCp-series).

30 Higher eukaryotic tissue culture cells are normally the preferred host cells for expression of the functionally active interleukin protein. In principle, any higher eukaryotic tissue culture cell line is workable, e.g., insect baculovirus expression systems,  
35 whether from an invertebrate or vertebrate source. However, mammalian cells are preferred. Transformation or transfection and propagation of such cells has become

a routine procedure. Examples of useful cell lines include HeLa cells, Chinese hamster ovary (CHO) cell lines, baby rat kidney (BRK) cell lines, insect cell lines, bird cell lines, and monkey (COS) cell lines.

5 Expression vectors for such cell lines usually include an origin of replication, a promoter, a translation initiation site, RNA splice sites (if genomic DNA is used), a polyadenylation site, and a transcription termination site. These vectors also usually contain a

10 selection gene or amplification gene. Suitable expression vectors may be plasmids, viruses, or retroviruses carrying promoters derived, e.g., from such sources as from adenovirus, SV40, parvoviruses, vaccinia virus, or cytomegalovirus. Representative examples of

15 suitable expression vectors include pCDNA1; pCD, see Okayama, et al. (1985) Mol. Cell Biol. 5:1136-1142; pMCIneo PolyA, see Thomas, et al. (1987) Cell 51:503-512; and a baculovirus vector such as pAC 373 or pAC 610.

For secreted proteins, an open reading frame usually

20 encodes a polypeptide that consists of a mature or secreted product covalently linked at its N-terminus to a signal peptide. The signal peptide is cleaved prior to secretion of the mature, or active, polypeptide. The cleavage site can be predicted with a high degree of

25 accuracy from empirical rules, e.g., von-Heijne (1986) Nucleic Acids Research 14:4683-4690, and the precise amino acid composition of the signal peptide does not appear to be critical to its function, e.g., Randall, et al. (1989) Science 243:1156-1159; Kaiser et al. (1987)

30 Science 235:312-317.

It will often be desired to express these polypeptides in a system which provides a specific or defined glycosylation pattern. In this case, the usual pattern will be that provided naturally by the expression

35 system. However, the pattern will be modifiable by exposing the polypeptide, e.g., an unglycosylated form, to appropriate glycosylating proteins introduced into a

heterologous expression system. For example, the receptor gene may be co-transformed with one or more genes encoding mammalian or other glycosylating enzymes. Using this approach, certain mammalian glycosylation patterns will be achievable in prokaryote or other cells.

The source of DTLR can be a eukaryotic or prokaryotic host expressing recombinant DTLR, such as is described above. The source can also be a cell line such as mouse Swiss 3T3 fibroblasts, but other mammalian cell lines are also contemplated by this invention, with the preferred cell line being from the human species.

Now that the sequences are known, the primate DTLRs, fragments, or derivatives thereof can be prepared by conventional processes for synthesizing peptides. These include processes such as are described in Stewart and Young (1984) Solid Phase Peptide Synthesis, Pierce Chemical Co., Rockford, IL; Bodanszky and Bodanszky (1984) The Practice of Peptide Synthesis, Springer-Verlag, New York; and Bodanszky (1984) The Principles of Peptide Synthesis, Springer-Verlag, New York; all of each which are incorporated herein by reference. For example, an azide process, an acid chloride process, an acid anhydride process, a mixed anhydride process, an active ester process (e.g., p-nitrophenyl ester, N-hydroxysuccinimide ester, or cyanomethyl ester), a carbodiimidazole process, an oxidative-reductive process, or a dicyclohexylcarbodiimide (DCCD)/additive process can be used. Solid phase and solution phase syntheses are both applicable to the foregoing processes. Similar techniques can be used with partial DTLR sequences.

The DTLR proteins, fragments, or derivatives are suitably prepared in accordance with the above processes as typically employed in peptide synthesis, generally either by a so-called stepwise process which comprises condensing an amino acid to the terminal amino acid, one by one in sequence, or by coupling peptide fragments to

the terminal amino acid. Amino groups that are not being used in the coupling reaction typically must be protected to prevent coupling at an incorrect location.

If a solid phase synthesis is adopted, the C-terminal amino acid is bound to an insoluble carrier or support through its carboxyl group. The insoluble carrier is not particularly limited as long as it has a binding capability to a reactive carboxyl group. Examples of such insoluble carriers include halomethyl resins, such as chloromethyl resin or bromomethyl resin, hydroxymethyl resins, phenol resins, tert-alkyloxycarbonylhydrazidated resins, and the like.

An amino group-protected amino acid is bound in sequence through condensation of its activated carboxyl group and the reactive amino group of the previously formed peptide or chain, to synthesize the peptide step by step. After synthesizing the complete sequence, the peptide is split off from the insoluble carrier to produce the peptide. This solid-phase approach is generally described by Merrifield, et al. (1963) in J. Am. Chem. Soc. 85:2149-2156, which is incorporated herein by reference.

The prepared protein and fragments thereof can be isolated and purified from the reaction mixture by means of peptide separation, for example, by extraction, precipitation, electrophoresis, various forms of chromatography, and the like. The receptors of this invention can be obtained in varying degrees of purity depending upon desired uses. Purification can be accomplished by use of the protein purification techniques disclosed herein, see below, or by the use of the antibodies herein described in methods of immunoabsorbant affinity chromatography. This immunoabsorbant affinity chromatography is carried out by first linking the antibodies to a solid support and then contacting the linked antibodies with solubilized lysates of appropriate cells, lysates of other cells expressing

the receptor, or lysates or supernatants of cells producing the protein as a result of DNA techniques, see below.

Generally, the purified protein will be at least  
5 about 40% pure, ordinarily at least about 50% pure, usually at least about 60% pure, typically at least about 70% pure, more typically at least about 80% pure, preferable at least about 90% pure and more preferably at least about 95% pure, and in particular embodiments, 97%-  
10 99% or more. Purity will usually be on a weight basis, but can also be on a molar basis. Different assays will be applied as appropriate.

#### VI. Antibodies

15 Antibodies can be raised to the various mammalian, e.g., primate DTLR proteins and fragments thereof, both in naturally occurring native forms and in their recombinant forms, the difference being that antibodies to the active receptor are more likely to recognize  
20 epitopes which are only present in the native conformations. Denatured antigen detection can also be useful in, e.g., Western analysis. Anti-idiotypic antibodies are also contemplated, which would be useful as agonists or antagonists of a natural receptor or an  
25 antibody.

Antibodies, including binding fragments and single chain versions, against predetermined fragments of the protein can be raised by immunization of animals with conjugates of the fragments with immunogenic proteins.  
30 Monoclonal antibodies are prepared from cells secreting the desired antibody. These antibodies can be screened for binding to normal or defective protein, or screened for agonistic or antagonistic activity. These monoclonal antibodies will usually bind with at least a  $K_D$  of about  
35 1 mM, more usually at least about 300  $\mu$ M, typically at least about 100 $\mu$ M, more typically at least about 30  $\mu$ M,

preferably at least about 10  $\mu$ M, and more preferably at least about 3  $\mu$ M or better.

The antibodies, including antigen binding fragments, of this invention can have significant diagnostic or therapeutic value. They can be potent antagonists that bind to the receptor and inhibit binding to ligand or inhibit the ability of the receptor to elicit a biological response, e.g., act on its substrate. They also can be useful as non-neutralizing antibodies and can be coupled to toxins or radionuclides to bind producing cells, or cells localized to the source of the interleukin. Further, these antibodies can be conjugated to drugs or other therapeutic agents, either directly or indirectly by means of a linker.

The antibodies of this invention can also be useful in diagnostic applications. As capture or non-neutralizing antibodies, they might bind to the receptor without inhibiting ligand or substrate binding. As neutralizing antibodies, they can be useful in competitive binding assays. They will also be useful in detecting or quantifying ligand. They may be used as reagents for Western blot analysis, or for immunoprecipitation or immunopurification of the respective protein.

Protein fragments may be joined to other materials, particularly polypeptides, as fused or covalently joined polypeptides to be used as immunogens. Mammalian DTLR and its fragments may be fused or covalently linked to a variety of immunogens, such as keyhole limpet hemocyanin, bovine serum albumin, tetanus toxoid, etc. See Microbiology, Hoeber Medical Division, Harper and Row, 1969; Landsteiner (1962) Specificity of Serological Reactions, Dover Publications, New York; and Williams, et al. (1967) Methods in Immunology and Immunochemistry, Vol. 1, Academic Press, New York; each of which are incorporated herein by reference, for descriptions of methods of preparing polyclonal antisera. A typical



method involves hyperimmunization of an animal with an antigen. The blood of the animal is then collected shortly after the repeated immunizations and the gamma globulin is isolated.

- 5 In some instances, it is desirable to prepare monoclonal antibodies from various mammalian hosts, such as mice, rodents, primates, humans, etc. Description of techniques for preparing such monoclonal antibodies may be found in, e.g., Stites, et al. (eds) Basic and
- 10 Clinical Immunology (4th ed.), Lange Medical Publications, Los Altos, CA, and references cited therein; Harlow and Lane (1988) Antibodies: A Laboratory Manual, CSH Press; Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed) Academic Press, New York;
- 15 and particularly in Kohler and Milstein (1975) in Nature 256: 495-497, which discusses one method of generating monoclonal antibodies. Each of these references is incorporated herein by reference. Summarized briefly, this method involves injecting an animal with an
- 20 immunogen. The animal is then sacrificed and cells taken from its spleen, which are then fused with myeloma cells. The result is a hybrid cell or "hybridoma" that is capable of reproducing in vitro. The population of hybridomas is then screened to isolate individual clones,
- 25 each of which secrete a single antibody species to the immunogen. In this manner, the individual antibody species obtained are the products of immortalized and cloned single B cells from the immune animal generated in response to a specific site recognized on the immunogenic substance.
- 30 Other suitable techniques involve in vitro exposure of lymphocytes to the antigenic polypeptides or alternatively to selection of libraries of antibodies in phage or similar vectors. See, Huse, et al. (1989)
- 35 "Generation of a Large Combinatorial Library of the Immunoglobulin Repertoire in Phage Lambda," Science 246:1275-1281; and Ward, et al. (1989) Nature 341:544-

546, each of which is hereby incorporated herein by reference. The polypeptides and antibodies of the present invention may be used with or without modification, including chimeric or humanized antibodies.

5 Frequently, the polypeptides and antibodies will be labeled by joining, either covalently or non-covalently, a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific  
10 and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, chemiluminescent moieties, magnetic particles, and the like. Patents, teaching the use of such labels include U.S. Patent Nos.  
15 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241. Also, recombinant or chimeric immunoglobulins may be produced, see Cabilly, U.S. Patent No. 4,816,567; or made in transgenic mice, see Mendez, et al. (1997) Nature Genetics 15:146-156. These references  
20 are incorporated herein by reference.

The antibodies of this invention can also be used for affinity chromatography in isolating the DTLRs. Columns can be prepared where the antibodies are linked to a solid support, e.g., particles, such as agarose,  
25 Sephadex, or the like, where a cell lysate may be passed through the column, the column washed, followed by increasing concentrations of a mild denaturant, whereby the purified protein will be released. The protein may be used to purify antibody.

30 The antibodies may also be used to screen expression libraries for particular expression products. Usually the antibodies used in such a procedure will be labeled with a moiety allowing easy detection of presence of antigen by antibody binding.

35 Antibodies raised against a DTLR will also be used to raise anti-idiotypic antibodies. These will be useful in detecting or diagnosing various immunological

conditions related to expression of the protein or cells which express the protein. They also will be useful as agonists or antagonists of the ligand, which may be competitive inhibitors or substitutes for naturally occurring ligands.

A DTLR protein that specifically binds to or that is specifically immunoreactive with an antibody generated against a defined immunogen, such as an immunogen consisting of the amino acid sequence of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34, is typically determined in an immunoassay. The immunoassay typically uses a polyclonal antiserum which was raised, e.g., to a protein of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34. This antiserum is selected to have low crossreactivity against other IL-1R family members, e.g., DTLR1, preferably from the same species, and any such crossreactivity is removed by immunoabsorption prior to use in the immunoassay.

In order to produce antisera for use in an immunoassay, the protein of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34, or a combination thereof, is isolated as described herein. For example, recombinant protein may be produced in a mammalian cell line. An appropriate host, e.g., an inbred strain of mice such as balb/c, is immunized with the selected protein, typically using a standard adjuvant, such as Freund's adjuvant, and a standard mouse immunization protocol (see Harlow and Lane, supra). Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used as an immunogen. Polyclonal sera are collected and titered against the immunogen protein in an immunoassay, e.g., a solid phase immunoassay with the immunogen immobilized on a solid support. Polyclonal antisera with a titer of  $10^4$  or greater are selected and tested for their cross reactivity against other IL-1R family members, e.g., mouse DTLRs or human DTLR1, using a competitive binding

immunoassay such as the one described in Harlow and Lane, supra, at pages 570-573. Preferably at least two DTLR family members are used in this determination in conjunction with either or some of the human DTLR2-10.

5 These IL-1R family members can be produced as recombinant proteins and isolated using standard molecular biology and protein chemistry techniques as described herein.

Immunoassays in the competitive binding format can be used for the crossreactivity determinations. For  
10 example, the proteins of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34, or various fragments thereof, can be immobilized to a solid support. Proteins added to the assay compete with the binding of the antisera to the immobilized antigen. The ability of the above proteins  
15 to compete with the binding of the antisera to the immobilized protein is compared to the protein of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 and/or 34. The percent crossreactivity for the above proteins is calculated, using standard calculations. Those antisera  
20 with less than 10% crossreactivity with each of the proteins listed above are selected and pooled. The cross-reacting antibodies are then removed from the pooled antisera by immunoabsorbtion with the above-listed proteins.

25 The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein to the immunogen protein (e.g., the IL-1R like protein of SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 and/or 34). In order to make this  
30 comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required is less than twice the amount  
35 of the protein of the selected protein or proteins that is required, then the second protein is said to

specifically bind to an antibody generated to the immunogen.

It is understood that these DTLR proteins are members of a family of homologous proteins that comprise at least 10 so far identified genes. For a particular gene product, such as the DTLR2-10, the term refers not only to the amino acid sequences disclosed herein, but also to other proteins that are allelic, non-allelic or species variants. It also understood that the terms include nonnatural mutations introduced by deliberate mutation using conventional recombinant technology such as single site mutation, or by excising short sections of DNA encoding the respective proteins, or by substituting new amino acids, or adding new amino acids. Such minor alterations must substantially maintain the immunoidentity of the original molecule and/or its biological activity. Thus, these alterations include proteins that are specifically immunoreactive with a designated naturally occurring IL-1R related protein, for example, the DTLR proteins shown in SEQ ID NO: 4, 6, 26, 10, 12, 16, 18, 32, 22 or 34. The biological properties of the altered proteins can be determined by expressing the protein in an appropriate cell line and measuring the appropriate effect upon lymphocytes. Particular protein modifications considered minor would include conservative substitution of amino acids with similar chemical properties, as described above for the IL-1R family as a whole. By aligning a protein optimally with the protein of DTLR2-10 and by using the conventional immunoassays described herein to determine immunoidentity, one can determine the protein compositions of the invention.

#### VII. Kits and quantitation

Both naturally occurring and recombinant forms of the IL-1R like molecules of this invention are particularly useful in kits and assay methods. For example, these methods would also be applied to screening

for binding activity, e.g., ligands for these proteins. Several methods of automating assays have been developed in recent years so as to permit screening of tens of thousands of compounds per year. See, e.g., a BIOMEK  
5 automated workstation, Beckman Instruments, Palo Alto, California, and Fodor, et al. (1991) Science 251:767-773, which is incorporated herein by reference. The latter describes means for testing binding by a plurality of defined polymers synthesized on a solid substrate. The  
10 development of suitable assays to screen for a ligand or agonist/antagonist homologous proteins can be greatly facilitated by the availability of large amounts of purified, soluble DTLRs in an active state such as is provided by this invention.

15 Purified DTLR can be coated directly onto plates for use in the aforementioned ligand screening techniques. However, non-neutralizing antibodies to these proteins can be used as capture antibodies to immobilize the respective receptor on the solid phase, useful, e.g., in  
20 diagnostic uses.

This invention also contemplates use of DTLR2-10, fragments thereof, peptides, and their fusion products in a variety of diagnostic kits and methods for detecting the presence of the protein or its ligand.

25 Alternatively, or additionally, antibodies against the molecules may be incorporated into the kits and methods. Typically the kit will have a compartment containing either a defined DTLR peptide or gene segment or a reagent which recognizes one or the other. Typically,  
30 recognition reagents, in the case of peptide, would be a receptor or antibody, or in the case of a gene segment, would usually be a hybridization probe.

A preferred kit for determining the concentration of, e.g., DTLR4, a sample would typically comprise a  
35 labeled compound, e.g., ligand or antibody, having known binding affinity for DTLR4, a source of DTLR4 (naturally occurring or recombinant) as a positive control, and a

means for separating the bound from free labeled compound, for example a solid phase for immobilizing the DTLR4 in the test sample. Compartments containing reagents, and instructions, will normally be provided.

5       Antibodies, including antigen binding fragments, specific for mammalian DTLR or a peptide fragment, or receptor fragments are useful in diagnostic applications to detect the presence of elevated levels of ligand and/or its fragments. Diagnostic assays may be  
10 homogeneous (without a separation step between free reagent and antibody-antigen complex) or heterogeneous (with a separation step). Various commercial assays exist, such as radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), enzyme immunoassay (EIA),  
15 enzyme-multiplied immunoassay technique (EMIT), substrate-labeled fluorescent immunoassay (SLFIA) and the like. For example, unlabeled antibodies can be employed by using a second antibody which is labeled and which recognizes the antibody to DTLR4 or to a particular  
20 fragment thereof. These assays have also been extensively discussed in the literature. See, e.g., Harlow and Lane (1988) Antibodies: A Laboratory Manual, CSH., and Coligan (Ed.) (1991) and periodic supplements, Current Protocols In Immunology Greene/Wiley, New York.

25       Anti-idiotypic antibodies may have similar use to serve as agonists or antagonists of DTLR4. These should be useful as therapeutic reagents under appropriate circumstances.

      Frequently, the reagents for diagnostic assays are  
30 supplied in kits, so as to optimize the sensitivity of the assay. For the subject invention, depending upon the nature of the assay, the protocol, and the label, either labeled or unlabeled antibody, or labeled ligand is provided. This is usually in conjunction with other  
35 additives, such as buffers, stabilizers, materials necessary for signal production such as substrates for enzymes, and the like. Preferably, the kit will also

contain instructions for proper use and disposal of the contents after use. Typically the kit has compartments for each useful reagent, and will contain instructions for proper use and disposal of reagents. Desirably, the reagents are provided as a dry lyophilized powder, where the reagents may be reconstituted in an aqueous medium having appropriate concentrations for performing the assay.

The aforementioned constituents of the diagnostic assays may be used without modification or may be modified in a variety of ways. For example, labeling may be achieved by covalently or non-covalently joining a moiety which directly or indirectly provides a detectable signal. In any of these assays, a test compound, DTLR, or antibodies thereto can be labeled either directly or indirectly. Possibilities for direct labeling include label groups: radiolabels such as  $^{125}\text{I}$ , enzymes (U.S. Pat. No. 3,645,090) such as peroxidase and alkaline phosphatase, and fluorescent labels (U.S. Pat. No. 3,940,475) capable of monitoring the change in fluorescence intensity, wavelength shift, or fluorescence polarization. Both of the patents are incorporated herein by reference. Possibilities for indirect labeling include biotinylation of one constituent followed by binding to avidin coupled to one of the above label groups.

There are also numerous methods of separating the bound from the free ligand, or alternatively the bound from the free test compound. The DTLR can be immobilized on various matrixes followed by washing. Suitable matrices include plastic such as an ELISA plate, filters, and beads. Methods of immobilizing the receptor to a matrix include, without limitation, direct adhesion to plastic, use of a capture antibody, chemical coupling, and biotin-avidin. The last step in this approach involves the precipitation of antibody/antigen complex by any of several methods including those utilizing, e.g.,



an organic solvent such as polyethylene glycol or a salt such as ammonium sulfate. Other suitable separation techniques include, without limitation, the fluorescein antibody magnetizable particle method described in Rattle, et al. (1984) Clin. Chem. 30(9):1457-1461, and the double antibody magnetic particle separation as described in U.S. Pat. No. 4,659,678, each of which is incorporated herein by reference.

The methods for linking protein or fragments to various labels have been extensively reported in the literature and do not require detailed discussion here. Many of the techniques involve the use of activated carboxyl groups either through the use of carbodiimide or active esters to form peptide bonds, the formation of thioethers by reaction of a mercapto group with an activated halogen such as chloroacetyl, or an activated olefin such as maleimide, for linkage, or the like. Fusion proteins will also find use in these applications.

Another diagnostic aspect of this invention involves use of oligonucleotide or polynucleotide sequences taken from the sequence of a DTLR. These sequences can be used as probes for detecting levels of the respective DTLR in patients suspected of having an immunological disorder. The preparation of both RNA and DNA nucleotide sequences, the labeling of the sequences, and the preferred size of the sequences has received ample description and discussion in the literature. Normally an oligonucleotide probe should have at least about 14 nucleotides, usually at least about 18 nucleotides, and the polynucleotide probes may be up to several kilobases. Various labels may be employed, most commonly radionuclides, particularly  $^{32}\text{P}$ . However, other techniques may also be employed, such as using biotin modified nucleotides for introduction into a polynucleotide. The biotin then serves as the site for binding to avidin or antibodies, which may be labeled with a wide variety of labels, such as radionuclides,

fluorescers, enzymes, or the like. Alternatively, antibodies may be employed which can recognize specific duplexes, including DNA duplexes, RNA duplexes, DNA-RNA hybrid duplexes, or DNA-protein duplexes. The antibodies in turn may be labeled and the assay carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected. The use of probes to the novel anti-sense RNA may be carried out in any conventional techniques such as nucleic acid hybridization, plus and minus screening, recombinational probing, hybrid released translation (HRT), and hybrid arrested translation (HART). This also includes amplification techniques such as polymerase chain reaction (PCR).

Diagnostic kits which also test for the qualitative or quantitative presence of other markers are also contemplated. Diagnosis or prognosis may depend on the combination of multiple indications used as markers. Thus, kits may test for combinations of markers. See, e.g., Viallet, et al. (1989) Progress in Growth Factor Res. 1:89-97.

#### VIII. Therapeutic Utility

This invention provides reagents with significant therapeutic value. The DTLRs (naturally occurring or recombinant), fragments thereof, mutein receptors, and antibodies, along with compounds identified as having binding affinity to the receptors or antibodies, should be useful in the treatment of conditions exhibiting abnormal expression of the receptors or their ligands. Such abnormality will typically be manifested by immunological disorders. Additionally, this invention should provide therapeutic value in various diseases or disorders associated with abnormal expression or abnormal triggering of response to the ligand. The Toll ligands have been suggested to be involved in morphologic

development, e.g., dorso-ventral polarity determination, and immune responses, particularly the primitive innate responses. See, e.g., Sun, et al. (1991) Eur. J. Biochem. 196:247-254; Hultmark (1994) Nature 367:116-117.

- 5       Recombinant DTLRs, muteins, agonist or antagonist antibodies thereto, or antibodies can be purified and then administered to a patient. These reagents can be combined for therapeutic use with additional active ingredients, e.g., in conventional pharmaceutically
- 10   acceptable carriers or diluents, along with physiologically innocuous stabilizers and excipients. These combinations can be sterile, e.g., filtered, and placed into dosage forms as by lyophilization in dosage vials or storage in stabilized aqueous preparations.
- 15   This invention also contemplates use of antibodies or binding fragments thereof which are not complement binding.

- Ligand screening using DTLR or fragments thereof can be performed to identify molecules having binding
- 20   affinity to the receptors. Subsequent biological assays can then be utilized to determine if a putative ligand can provide competitive binding, which can block intrinsic stimulating activity. Receptor fragments can be used as a blocker or antagonist in that it blocks the
- 25   activity of ligand. Likewise, a compound having intrinsic stimulating activity can activate the receptor and is thus an agonist in that it simulates the activity of ligand, e.g., inducing signaling. This invention further contemplates the therapeutic use of antibodies to
- 30   DTLRs as antagonists.

- The quantities of reagents necessary for effective therapy will depend upon many different factors, including means of administration, target site, physiological state of the patient, and other medicants
- 35   administered. Thus, treatment dosages should be titrated to optimize safety and efficacy. Typically, dosages used in vitro may provide useful guidance in the amounts

useful for in situ administration of these reagents. Animal testing of effective doses for treatment of particular disorders will provide further predictive indication of human dosage. Various considerations are described, e.g., in Gilman, et al. (eds) (1990) Goodman and Gilman's: The Pharmacological Bases of Therapeutics, 8th Ed., Pergamon Press; and Remington's Pharmaceutical Sciences, (current edition), Mack Publishing Co., Easton, Penn.; each of which is hereby incorporated herein by reference. Methods for administration are discussed therein and below, e.g., for oral, intravenous, intraperitoneal, or intramuscular administration, transdermal diffusion, and others. Pharmaceutically acceptable carriers will include water, saline, buffers, and other compounds described, e.g., in the Merck Index, Merck & Co., Rahway, New Jersey. Because of the likely high affinity binding, or turnover numbers, between a putative ligand and its receptors, low dosages of these reagents would be initially expected to be effective. And the signaling pathway suggests extremely low amounts of ligand may have effect. Thus, dosage ranges would ordinarily be expected to be in amounts lower than 1 mM concentrations, typically less than about 10  $\mu$ M concentrations, usually less than about 100 nM, preferably less than about 10 pM (picomolar), and most preferably less than about 1 fM (femtomolar), with an appropriate carrier. Slow release formulations, or slow release apparatus will often be utilized for continuous administration.

DTLRs, fragments thereof, and antibodies or its fragments, antagonists, and agonists, may be administered directly to the host to be treated or, depending on the size of the compounds, it may be desirable to conjugate them to carrier proteins such as ovalbumin or serum albumin prior to their administration. Therapeutic formulations may be administered in any conventional dosage formulation. While it is possible for the active

ingredient to be administered alone, it is preferable to present it as a pharmaceutical formulation. Formulations comprise at least one active ingredient, as defined above, together with one or more acceptable carriers thereof. Each carrier must be both pharmaceutically and physiologically acceptable in the sense of being compatible with the other ingredients and not injurious to the patient. Formulations include those suitable for oral, rectal, nasal, or parenteral (including subcutaneous, intramuscular, intravenous and intradermal) administration. The formulations may conveniently be presented in unit dosage form and may be prepared by any methods well known in the art of pharmacy. See, e.g., Gilman, et al. (eds) (1990) Goodman and Gilman's: The Pharmacological Bases of Therapeutics, 8th Ed., Pergamon Press; and Remington's Pharmaceutical Sciences (current edition), Mack Publishing Co., Easton, Penn.; Avis, et al. (eds. 1993) Pharmaceutical Dosage Forms: Parenteral Medications Dekker, NY; Lieberman, et al. (eds. 1990) Pharmaceutical Dosage Forms: Tablets Dekker, NY; and Lieberman, et al. (eds. 1990) Pharmaceutical Dosage Forms: Disperse Systems Dekker, NY. The therapy of this invention may be combined with or used in association with other therapeutic agents, particularly agonists or antagonists of other IL-1 family members.

#### IX. Ligands

The description of the Toll receptors herein provide means to identify ligands, as described above. Such ligand should bind specifically to the respective receptor with reasonably high affinity. Various constructs are made available which allow either labeling of the receptor to detect its ligand. For example, directly labeling DTLR, fusing onto it markers for secondary labeling, e.g., FLAG or other epitope tags, etc., will allow detection of receptor. This can be histological, as an affinity method for biochemical

purification, or labeling or selection in an expression cloning approach. A two-hybrid selection system may also be applied making appropriate constructs with the available DTLR sequences. See, e.g., Fields and Song  
5 (1989) Nature 340:245-246.

Generally, descriptions of DTLRs will be analogously applicable to individual specific embodiments directed to DTLR2, DTLR3, DTLR4, DTLR5, DTLR6, DTLR7, DTLR8, DTLR9, and/or DTLR10 reagents and compositions.

10 The broad scope of this invention is best understood with reference to the following examples, which are not intended to limit the inventions to the specific embodiments.

## 15 EXAMPLES

### I. General Methods

Some of the standard methods are described or referenced, e.g., in Maniatis, et al. (1982) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor Press; Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual, (2d ed.), vols 1-3, CSH Press, NY; Ausubel, et al., Biology, Greene Publishing Associates, Brooklyn, NY; or Ausubel, et al. (1987 and Supplements) Current Protocols in Molecular Biology, Greene/Wiley, New York. Methods for protein purification include such methods as ammonium sulfate precipitation, column chromatography, electrophoresis, centrifugation, crystallization, and  
20 others. See, e.g., Ausubel, et al. (1987 and periodic supplements); Coligan, et al. (ed. 1996) and periodic supplements, Current Protocols In Protein Science Greene/Wiley, New York; Deutscher (1990) "Guide to Protein Purification" in Methods in Enzymology, vol. 182,  
25 and other volumes in this series; and manufacturer's literature on use of protein purification products, e.g., Pharmacia, Piscataway, N.J., or Bio-Rad, Richmond, CA.  
35

- Combination with recombinant techniques allow fusion to appropriate segments, e.g., to a FLAG sequence or an equivalent which can be fused via a protease-removable sequence. See, e.g., Hochuli (1989) Chemische Industrie 12:69-70; Hochuli (1990) "Purification of Recombinant Proteins with Metal Chelate Absorbent" in Setlow (ed.) Genetic Engineering, Principle and Methods 12:87-98, Plenum Press, N.Y.; and Crowe, et al. (1992) QIAexpress: The High Level Expression & Protein Purification System
- 10 QUIAGEN, Inc., Chatsworth, CA.

- Standard immunological techniques and assays are described, e.g., in Hertenzenberg, et al. (eds. 1996) Weir's Handbook of Experimental Immunology vols. 1-4, Blackwell Science; Coligan (1991) Current Protocols in Immunology Wiley/Greene, NY; and Methods in Enzymology volumes. 70, 73, 74, 84, 92, 93, 108, 116, 121, 132, 150, 162, and 163.
- 15

- Assays for vascular biological activities are well known in the art. They will cover angiogenic and angiostatic activities in tumor, or other tissues, e.g., arterial smooth muscle proliferation (see, e.g., Koyoma, et al. (1996) Cell 87:1069-1078), monocyte adhesion to vascular epithelium (see McEvoy, et al. (1997) J. Exp. Med. 185:2069-2077), etc. See also Ross (1993) Nature 362:801-809; Rekhter and Gordon (1995) Am. J. Pathol. 147:668-677; Thyberg, et al. (1990) Atherosclerosis 10:966-990; and Gumbiner (1996) Cell 84:345-357.
- 20
- 25

- Assays for neural cell biological activities are described, e.g., in Wouterlood (ed. 1995) Neuroscience Protocols modules 10, Elsevier; Methods in Neurosciences Academic Press; and Neuromethods Humana Press, Totowa, NJ. Methodology of developmental systems is described, e.g., in Meisami (ed.) Handbook of Human Growth and Developmental Biology CRC Press; and Chrispeels (ed.) Molecular Techniques and Approaches in Developmental Biology Interscience.
- 30
- 35

Computer sequence analysis is performed, e.g., using available software programs, including those from the GCG (U. Wisconsin) and GenBank sources. Public sequence databases were also used, e.g., from GenBank, NCBI, EMBO, and others.

Many techniques applicable to IL-10 receptors may be applied to DTLRs, as described, e.g., in USSN 08/110,683 (IL-10 receptor), which is incorporated herein by reference for all purposes.

## II. Novel Family of Human Receptors

Abbreviations: DTLR, Toll-like receptor; IL-1R, interleukin-1 receptor; TH, Toll homology; LRR, leucine-rich repeat; EST, expressed sequence tag; STS, sequence tagged site; FISH, fluorescence in situ hybridization.

The discovery of sequence homology between the cytoplasmic domains of *Drosophila* Toll and human interleukin-1 (IL-1) receptors has sown the conviction that both molecules trigger related signaling pathways tied to the nuclear translocation of Rel-type transcription factors. This conserved signaling scheme governs an evolutionarily ancient immune response in both insects and vertebrates. We report the molecular cloning of a novel class of putative human receptors with a protein architecture that is closely similar to *Drosophila* Toll in both intra- and extra-cellular segments. Five human Toll-like receptors, designated DTLRs 1-5, are likely the direct homologs of the fly molecule, and as such could constitute an important and unrecognized component of innate immunity in humans; intriguingly, the evolutionary retention of DTLRs in vertebrates may indicate another role, akin to Toll in the dorso-ventralization of the *Drosophila* embryo, as regulators of early morphogenetic patterning. Multiple tissue mRNA blots indicate markedly different patterns of



expression for the human DTLRs. Using fluorescence in situ hybridization and Sequence-Tagged Site database analyses, we also show that the cognate DTLR genes reside on chromosomes 4 (DTLRs 1, 2, and 3), 9 (DTLR4), and 1  
5 (DTLR5). Structure prediction of the aligned Toll-homology (TH) domains from varied insect and human DTLRs, vertebrate IL-1 receptors, and MyD88 factors, and plant disease resistance proteins, recognizes a parallel  $\beta/\alpha$  fold with an acidic active site; a similar structure  
10 notably recurs in a class of response regulators broadly involved in transducing sensory information in bacteria.

The seeds of the morphogenetic gulf that so dramatically separates flies from humans are planted in  
15 familiar embryonic shapes and patterns, but give rise to very different cell complexities. DeRobertis and Sasai (1996) Nature 380:37-40; and Arendt and Nübler-Jung (1997) Mech. Develop. 61:7-21. This divergence of developmental plans between insects and vertebrates is  
20 choreographed by remarkably similar signaling pathways, underscoring a greater conservation of protein networks and biochemical mechanisms from unequal gene repertoires. Miklos and Rubin (1996) Cell 86:521-529; and Chothia (1994) Develop. 1994 Suppl., 27-33. A powerful way to  
25 chart the evolutionary design of these regulatory pathways is by inferring their likely molecular components (and biological functions) through interspecies comparisons of protein sequences and structures. Miklos and Rubin (1996) Cell 86:521-529;  
30 Chothia (1994) Develop. 1994 Suppl., 27-33 (3-5); and Banfi, et al. (1996) Nature Genet. 13:167-174.

A universally critical step in embryonic development is the specification of body axes, either born from innate asymmetries or triggered by external cues.  
35 DeRobertis and Sasai (1996) Nature 380:37-40; and Arendt and Nübler-Jung (1997) Mech. Develop. 61:7-21. As a model system, particular attention has been focused on

the phylogenetic basis and cellular mechanisms of dorsoventral polarization . DeRobertis and Sasai (1996) Nature 380:37-40; and Arendt and Nübler-Jung (1997) Mech. Develop. 61:7-21. A prototype molecular strategy for

5 this transformation has emerged from the Drosophila embryo, where the sequential action of a small number of genes results in a ventralizing gradient of the transcription factor Dorsal. St. Johnston and Nüsslein-Volhard (1992) Cell 68:201-219; and Morisato and Anderson

10 (1995) Ann. Rev. Genet. 29:371-399.

This signaling pathway centers on Toll, a transmembrane receptor that transduces the binding of a maternally-secreted ventral factor, Spätzle, into the cytoplasmic engagement of Tube, an accessory molecule,

15 and the activation of Pelle, a Ser/Thr kinase that catalyzes the dissociation of Dorsal from the inhibitor Cactus and allows migration of Dorsal to ventral nuclei (Morisato and Anderson (1995) Ann. Rev. Genet. 29:371-399; and Belvin and Anderson (1996) Ann. Rev. Cell

20 Develop. Biol. 12:393-416. The Toll pathway also controls the induction of potent antimicrobial factors in the adult fly (Lemaitre, et al. (1996) Cell 86:973-983); this role in Drosophila immune defense strengthens mechanistic parallels to IL-1 pathways that govern a host

25 of immune and inflammatory responses in vertebrates. Belvin and Anderson (1996) Ann. Rev. Cell Develop. Biol. 12:393-416; and Wasserman (1993) Molec. Biol. Cell 4:767-771. A Toll-related cytoplasmic domain in IL-1 receptors directs the binding of a Pelle-like kinase, IRAK, and the

30 activation of a latent NF- $\kappa$ B/I- $\kappa$ B complex that mirrors the embrace of Dorsal and Cactus. Belvin and Anderson (1996) Ann. Rev. Cell Develop. Biol. 12:393-416; and Wasserman (1993) Molec. Biol. Cell 4:767-771.

We describe the cloning and molecular

35 characterization of four new Toll-like molecules in humans, designated DTLRs 2-5 (following Chiang & Beachy (1994) Mech. Develop. 47:225-239), that reveal a receptor

family more closely tied to *Drosophila* Toll homologs than to vertebrate IL-1 receptors. The DTLR sequences are derived from human ESTs; these partial cDNAs were used to draw complete expression profiles in human tissues for the five DTLRs, map the chromosomal locations of cognate genes, and narrow the choice of cDNA libraries for full-length cDNA retrievals. Spurred by other efforts (Banfi, et al. (1996) Nature Genet. 13:167-174; and Wang, et al. (1996) J. Biol. Chem. 271:4468-4476), we are assembling, by structural conservation and molecular parsimony, a biological system in humans that is the counterpart of a compelling regulatory scheme in *Drosophila*. In addition, a biochemical mechanism driving Toll signaling is suggested by the proposed tertiary fold of the Toll-homology (TH) domain, a core module shared by DTLRs, a broad family of IL-1 receptors, mammalian MyD88 factors and plant disease resistance proteins. Mitcham, et al. (1996) J. Biol. Chem. 271:5777-5783; and Hardiman, et al. (1996) Oncogene 13:2467-2475. We propose that a signaling route coupling morphogenesis and primitive immunity in insects, plants, and animals (Belvin and Anderson (1996) Ann. Rev. Cell Develop. Biol. 12:393-416; and Wilson, et al. (1997) Curr. Biol. 7:175-178) may have roots in bacterial two-component pathways.

## Computational Analysis.

Human sequences related to insect DTLRs were identified from the EST database (dbEST) at the National Center for Biotechnology Information (NCBI) using the BLAST server (Altschul, et al. (1994) Nature Genet. 6:119-129). More sensitive pattern- and profile-based methods (Bork and Gibson (1996) Meth. Enzymol. 266:162-184) were used to isolate the signaling domains of the DTLR family that are shared with vertebrate and plant proteins present in nonredundant databases. The progressive alignment of DTLR intra- or extracellular domain sequences was carried out by ClustalW (Thompson,

et al. (1994) Nucleic Acids Res. 22:4673-4680); this program also calculated the branching order of aligned sequences by the Neighbor-Joining algorithm (5000 bootstrap replications provided confidence values for the tree groupings).

Conserved alignment patterns, discerned at several degrees of stringency, were drawn by the Consensus program (internet URL <http://www.bork.embl-heidelberg.de/Alignment/consensus.html>). The PRINTS library of protein fingerprints (<http://www.biochem.ucl.ac.uk/bsm/dbbrowser/PRINTS/PRINTS.html>) (Attwood, et al. (1997) Nucleic Acids Res. 25:212-217) reliably identified the myriad leucine-rich repeats (LRRs) present in the extracellular segments of DTLRs with a compound motif (PRINTS code Leurichrpt) that flexibly matches N- and C-terminal features of divergent LRRs. Two prediction algorithms whose three-state accuracy is above 72% were used to derive a consensus secondary structure for the intracellular domain alignment, as a bridge to fold recognition efforts (Fischer, et al. (1996) FASEB J. 10:126-136). Both the neural network program PHD (Rost and Sander (1994) Proteins 19:55-72) and the statistical prediction method DSC (King and Sternberg (1996) Protein Sci. 5:2298-2310) have internet servers (URLs [http://www.embl-heidelberg.de/predictprotein/phd\\_pred.html](http://www.embl-heidelberg.de/predictprotein/phd_pred.html) and [http://bonsai.lif.icnet.uk/bmm/dsc/dsc\\_read\\_align.html](http://bonsai.lif.icnet.uk/bmm/dsc/dsc_read_align.html), respectively). The intracellular region encodes the THD region discussed, e.g., in Hardiman, et al. (1996) Oncogene 13:2467-2475; and Rock, et al. (1998) Proc. Nat'l Acad. Sci. USA 95:588-593, each of which is incorporated herein by reference. This domain is very important in the mechanism of signaling by the receptors, which transfers a phosphate group to a substrate.

Cloning of full-length human DTLR cDNAs.

PCR primers derived from the Toll-like Humrsc786 sequence (Genbank accession code D13637) (Nomura, et al. (1994) DNA Res 1:27-35) were used to probe a human erythroleukemic, TF-1 cell line-derived cDNA library (Kitamura, et al. (1989) Blood 73:375-380) to yield the DTLR1 cDNA sequence. The remaining DTLR sequences were flagged from dbEST, and the relevant EST clones obtained from the I.M.A.G.E. consortium (Lennon, et al. (1996) Genomics 33:151-152) via Research Genetics (Huntsville, AL): CloneID#'s 80633 and 117262 (DTLR2), 144675 (DTLR3), 202057 (DTLR4) and 277229 (DTLR5). Full length cDNAs for human DTLRs 2-4 were cloned by DNA hybridization screening of  $\lambda$ gt10 phage, human adult lung, placenta, and fetal liver 5'-Stretch Plus cDNA libraries (Clontech), respectively; the DTLR5 sequence is derived from a human multiple-sclerosis plaque EST. All positive clones were sequenced and aligned to identify individual DTLR ORFs: DTLR1 (2366 bp clone, 786 aa ORF), DTLR2 (2600 bp, 784 aa), DTLR3 (3029 bp, 904 aa), DTLR4 (3811 bp, 879 aa) and DTLR5 (1275 bp, 370 aa). Probes for DTLR3 and DTLR4 hybridizations were generated by PCR using human placenta (Stratagene) and adult liver (Clontech) cDNA libraries as templates, respectively; primer pairs were derived from the respective EST sequences. PCR reactions were conducted using T. aquaticus Taqplus DNA polymerase (Stratagene) under the following conditions: 1 x (94° C, 2 min) 30 x (55° C, 20 sec; 72° C 30 sec; 94° C 20 sec), 1 x (72° C, 8 min). For DTLR2 full-length cDNA screening, a 900 bp fragment generated by EcoRI/XbaI digestion of the first EST clone (ID# 80633) was used as a probe.

mRNA blots and chromosomal localization.

Human multiple tissue (Cat# 1, 2) and cancer cell line blots (Cat# 7757-1), containing approximately 2  $\mu$ g of poly(A)<sup>+</sup> RNA per lane, were purchased from Clontech (Palo Alto, CA). For DTLRs 1-4, the isolated full-length

- cDNAs served as probes, for DTLR5 the EST clone (ID #277229) plasmid insert was used. Briefly, the probes were radiolabeled with [ $\alpha$ - $^{32}$ P] dATP using the Amersham Rediprime random primer labeling kit (RPN1633).
- 5 Prehybridization and hybridizations were performed at 65° C in 0.5 M Na<sub>2</sub>HPO<sub>4</sub>, 7% SDS, 0.5 M EDTA (pH 8.0). All stringency washes were conducted at 65° C with two initial washes in 2 x SSC, 0.1% SDS for 40 min followed by a subsequent wash in 0.1 x SSC, 0.1% SDS for 20 min.
- 10 Membranes were then exposed at -70° C to X-Ray film (Kodak) in the presence of intensifying screens. More detailed studies by cDNA library Southernblots (14) were performed with selected human DTLR clones to examine their expression in hemopoietic cell subsets.
- 15 Human chromosomal mapping was conducted by the method of fluorescence in situ hybridization (FISH) as described in Heng and Tsui (1994) Meth. Molec. Biol. 33:109-122, using the various full-length (DTLRs 2-4) or partial (DTLR5) cDNA clones as probes. These analyses
- 20 were performed as a service by SeeDNA Biotech Inc. (Ontario, Canada). A search for human syndromes (or mouse defects in syntenic loci) associated with the mapped DTLR genes was conducted in the Dysmorphic Human-Mouse Homology Database by internet server
- 25 ([http://www.hgmp.mrc.ac.uk/DHMH/hum\\_chromel.html](http://www.hgmp.mrc.ac.uk/DHMH/hum_chromel.html)).

Conserved architecture of insect and human DTLR ectodomains.

- The Toll family in *Drosophila* comprises at least
- 30 four distinct gene products: Toll, the prototype receptor involved in dorsoventral patterning of the fly embryo (Morisato and Anderson (1995) Ann. Rev. Genet. 29:371-399) and a second named '18 Wheeler' (18w) that may also be involved in early embryonic development (Chiang and
- 35 Beachy (1994) Mech. Develop. 47:225-239; Eldon, et al. (1994) Develop. 120:885-899); two additional receptors are predicted by incomplete, Toll-like ORFs downstream of

the male-specific-transcript (Mst) locus (Genbank code X67703) or encoded by the 'sequence-tagged-site' (STS) Dm2245 (Genbank code G01378) (Mitcham, et al. (1996) J. Biol. Chem. 271:5777-5783). The extracellular segments

5 of Toll and 18w are distinctively composed of imperfect, ~24 amino acid LRR motifs (Chiang and Beachy (1994) Mech. Develop. 47:225-239; and Eldon, et al. (1994) Develop. 120:885-899). Similar tandem arrays of LRRs commonly form the adhesive antennae of varied cell surface

10 molecules and their generic tertiary structure is presumed to mimic the horseshoe-shaped cradle of a ribonuclease inhibitor fold, where seventeen LRRs show a repeating  $\beta/\alpha$ -hairpin, 28 residue motif (Buchanan and Gay (1996) Prog. Biophys. Molec. Biol. 65:1-44). The

15 specific recognition of Spätzle by Toll may follow a model proposed for the binding of cystine-knot fold glycoprotein hormones by the multi-LRR ectodomains of serpentine receptors, using the concave side of the curved  $\beta$ -sheet (Kajava, et al. (1995) Structure 3:867-877); intriguingly, the pattern of cysteines in Spätzle, and an orphan Drosophila ligand, Trunk, predict a similar

20 cystine-knot tertiary structure (Belvin and Anderson (1996) Ann. Rev. Cell Develop. Biol. 12:393-416; and Casanova, et al. (1995) Genes Develop. 9:2539-2544).

25 The 22 and 31 LRR ectodomains of Toll and 18w, respectively (the Mst ORF fragment displays 16 LRRs), are most closely related to the comparable 18, 19, 24, and 22 LRR arrays of DTLRs 1-4 (the incomplete DTLR5 chain presently includes four membrane-proximal LRRs) by

30 sequence and pattern analysis (Altschul, et al. (1994) Nature Genet. 6:119-129; and Bork and Gibson (1996) Meth. Enzymol. 266:162-184) (Fig. 1). However, a striking difference in the human DTLR chains is the common loss of a ~90 residue cysteine-rich region that is variably

35 embedded in the ectodomains of Toll, 18w and the Mst ORF (distanced four, six and two LRRs, respectively, from the membrane boundary). These cysteine clusters are

bipartite, with distinct 'top' (ending an LRR) and 'bottom' (stacked atop an LRR) halves (Chiang and Beachy (1994) Mech. Develop. 47:225-239; Eldon, et al. (1994) Develop. 120:885-899; and Buchanan and Gay (1996) Prog. Biophys. Molec. Biol. 65:1-44); the 'top' module recurs in both Drosophila and human DTLRs as a conserved juxtamembrane spacer (Fig. 1). We suggest that the flexibly located cysteine clusters in Drosophila receptors (and other LRR proteins), when mated 'top' to 'bottom', form a compact module with paired termini that can be inserted between any pair of LRRs without altering the overall fold of DTLR ectodomains; analogous 'extruded' domains decorate the structures of other proteins (Russell (1994) Protein Engin. 7:1407-1410).

Molecular design of the TH signaling domain.

Sequence comparison of Toll and IL-1 type-I (IL-1R1) receptors has disclosed a distant resemblance of a ~200 amino acid cytoplasmic domain that presumably mediates signaling by similar Rel-type transcription factors. Belvin and Anderson (1996) Ann. Rev. Cell Develop. Biol. 12:393-416; and (Belvin and Anderson (1996) Ann. Rev. Cell Develop. Biol. 12:393-416; and Wasserman (1993) Molec. Biol. Cell 4:767-771). More recent additions to this functional paradigm include a pair of plant disease resistance proteins from tobacco and flax that feature an N-terminal TH module followed by nucleotide-binding (NTPase) and LRR segments (Wilson, et al. (1997) Curr. Biol. 7:175-178); by contrast, a 'death domain' preceeds the TH chain of MyD88, an intracellular myeloid differentiation marker (Mitcham, et al. (1996) J. Biol. Chem. 271:5777-5783; and Hardiman, et al. (1996) Oncogene 13:2467-2475) (Fig. 1). New IL-1-type receptors include IL-1R3, an accessory signaling molecule, and orphan receptors IL-1R4 (also called ST2/Fit-1/T1), IL-1R5 (IL-1R-related protein), and IL-1R6 (IL-1R-related protein-2) (Mitcham, et al. (1996) J. Biol. Chem. 271:5777-



5783;Hardiman, et al. (1996) Oncogene 13:2467-2475).

With the new human DTLR sequences, we have sought a structural definition of this evolutionary thread by analyzing the conformation of the common TH module: ten blocks of conserved sequence comprising 128 amino acids form the minimal TH domain fold; gaps in the alignment mark the likely location of sequence and length-variable loops (Fig. 2a).

Two prediction algorithms that take advantage of the patterns of conservation and variation in multiply aligned sequences, PHD (Rost and Sander (1994) Proteins 19:55-72) and DSC (King and Sternberg (1996) Protein Sci. 5:2298-2310), produced strong, concordant results for the TH signaling module (Fig. 2a). Each block contains a discrete secondary structural element: the imprint of alternating  $\beta$ -strands (labeled A-E) and  $\alpha$ -helices (numbered 1-5) is diagnostic of an  $\beta/\alpha$ -class fold with  $\alpha$ -helices on both faces of a parallel  $\beta$ -sheet. Hydrophobic  $\beta$ -strands A, C and D are predicted to form 'interior' staves in the  $\beta$ -sheet, while the shorter, amphipathic  $\beta$ -strands B and E resemble typical 'edge' units (Fig. 2a). This assignment is consistent with a strand order of B-A-C-D-E in the core  $\beta$ -sheet (Fig. 2b); fold comparison ('mapping') and recognition ('threading') programs (Fischer, et al. (1996) FASEB J. 10:126-136) strongly return this doubly wound  $\beta/\alpha$  topology. A surprising, functional prediction of this outline structure for the TH domain is that many of the conserved, charged residues in the multiple alignment map to the C-terminal end of the  $\beta$ -sheet: residue Asp16 (block numbering scheme - Fig. 2a) at the end of  $\beta$ A, Arg39 and Asp40 following  $\beta$ B, Glu75 in the first turn of  $\alpha$ 3, and the more loosely conserved Glu/Asp residues in the  $\beta$ D- $\alpha$ 4 loop, or after  $\beta$ E (Fig. 2a). The location of four other conserved residues (Asp7, Glu28, and the Arg57-Arg/Lys58 pair) is compatible with a salt bridge network at the opposite, N-terminal end of the  $\beta$ -sheet (Fig. 2a).

Signaling function depends on the structural integrity of the TH domain. Inactivating mutations or deletions within the module boundaries (Fig. 2a) have been catalogued for IL-1R1 and Toll. Heguy, et al. (1992) J. Biol. Chem. 267:2605-2609; Croston, et al. (1995) J. Biol. Chem. 270:16514-16517; Schneider, et al. (1991) Genes Develop. 5:797-807; Norris and Manley. (1992) Genes Develop. 6:1654-1667; Norris and Manley (1995) Genes Develop. 9:358-369; and Norris and Manley (1996) Genes Develop. 10:862-872. The human DTLR1-5 chains extending past the minimal TH domain (8, 0, 6, 22 and 18 residue lengths, respectively) are most closely similar to the stubby, 4 aa 'tail' of the Mst ORF. Toll and 18w display unrelated 102 and 207 residue tails (Fig. 2a) that may negatively regulate the signaling of the fused TH domains. Norris and Manley (1995) Genes Develop. 9:358-369; and Norris and Manley (1996) Genes Develop. 10:862-872.

The evolutionary relationship between the disparate proteins that carry the TH domain can best be discerned by a phylogenetic tree derived from the multiple alignment (Fig. 3). Four principal branches segregate the plant proteins, the MyD88 factors, IL-1 receptors and Toll-like molecules; the latter branch clusters the *Drosophila* and human DTLRs.

Chromosomal dispersal of human DTLR genes.

In order to investigate the genetic linkage of the nascent human DTLR gene family, we mapped the chromosomal loci of four of the five genes by FISH (Fig. 4). The DTLR1 gene has previously been charted by the human genome project: an STS database locus (dbSTS accession number G06709, corresponding to STS WI-7804 or SHGC-12827) exists for the Humrsc786 cDNA (Nomura, et al. (1994) DNA Res 1:27-35) and fixes the gene to chromosome 4 marker interval D4S1587-D42405 (50-56 cM) circa 4p14. This assignment has recently been corroborated by FISH

analysis. Taguchi, et al. (1996) Genomics 32:486-488. In the present work, we reliably assign the remaining DTLR genes to loci on chromosome 4q32 (DTLR2), 4q35 (DTLR3), 9q32-33 (DTLR4) and 1q33.3 (DTLR5). During the course of this work, an STS for the parent DTLR2 EST (cloneID # 80633) has been generated (dbSTS accession number T57791 for STS SHGC-33147) and maps to the chromosome 4 marker interval D4S424-D4S1548 (143-153 cM) at 4q32 -in accord with our findings. There is a ~50 cM gap between DTLR2 and DTLR3 genes on the long arm of chromosome 4.

DTLR genes are differentially expressed.

Both Toll and 18w have complex spatial and temporal patterns of expression in *Drosophila* that may point to functions beyond embryonic patterning. St. Johnston and Nüsslein-Volhard (1992) Cell 68:201-219; Morisato and Anderson (1995) Ann. Rev. Genet. 29:371-399; Belvin and Anderson (1996) Ann. Rev. Cell Develop. Biol. 12:393-416; Lemaitre, et al. (1996) Cell 86:973-983; Chiang and Beachy (1994) Mech. Develop. 47:225-239; and Eldon, et al. (1994) Develop. 120:885-899. We have examined the spatial distribution of DTLR transcripts by mRNA blot analysis with varied human tissue and cancer cell lines using radioabeled DTLR cDNAs (Fig. 5). DTLR1 is found to be ubiquitously expressed, and at higher levels than the other receptors. Presumably reflecting alternative splicing, 'short' 3.0 kB and 'long' 8.0 kB DTLR1 transcript forms are present in ovary and spleen, respectively (Fig. 5, panels A & B). A cancer cell mRNA panel also shows the prominent overexpression of DTLR1 in a Burkitt's Lymphoma Raji cell line (Fig. 5, panel C). DTLR2 mRNA is less widely expressed than DTLR1, with a 4.0 kB species detected in lung and a 4.4 kB transcript evident in heart, brain and muscle. The tissue distribution pattern of DTLR3 echoes that of DTLR2 (Fig. 5, panel E). DTLR3 is also present as two major

transcripts of approximately 4.0 and 6.0 kB in size, and the highest levels of expression are observed in placenta and pancreas. By contrast, DTLR4 and DTLR5 messages appear to be extremely tissue-specific. DTLR4 was  
5 detected only in placenta as a single transcript of ~7.0 kB in size. A faint 4.0 kB signal was observed for DTLR5 in ovary and peripheral blood monocytes.

Components of an evolutionarily ancient regulatory  
10 system.

The original molecular blueprints and divergent fates of signaling pathways can be reconstructed by comparative genomic approaches. Miklos and Rubin (1996) Cell 86:521-529; Chothia (1994) Develop. 1994 Suppl., 27-  
15 33; Banfi, et al. (1996) Nature Genet. 13:167-174; and Wang, et al. (1996) J. Biol. Chem. 271:4468-4476. We have used this logic to identify an emergent gene family in humans, encoding five receptor paralogs at present, DTLRs 1-5, that are the direct evolutionary counterparts  
20 of a *Drosophila* gene family headed by Toll (Figs. 1-3). The conserved architecture of human and fly DTLRs, conserved LRR ectodomains and intracellular TH modules (Fig. 1), intimates that the robust pathway coupled to Toll in *Drosophila* (6, 7) survives in vertebrates. The  
25 best evidence borrows from a reiterated pathway: the manifold IL-1 system and its repertoire of receptor-fused TH domains, IRAK, NF- $\kappa$ B and I- $\kappa$ B homologs (Belvin and Anderson (1996) Ann. Rev. Cell Develop. Biol. 12:393-416; Wasserman (1993) Molec. Biol. Cell 4:767-771; Hardiman,  
30 et al. (1996) Oncogene 13:2467-2475; and Cao, et al. (1996) Science 271:1128-1131); a Tube-like factor has also been characterized. It is not known whether DTLRs can productively couple to the IL-1R signaling machinery, or instead, a parallel set of proteins is used.  
35 Differently from IL-1 receptors, the LRR cradle of human DTLRs is predicted to retain an affinity for Spätzle/Trunk-related cystine-knot factors; candidate

DTLR ligands (called PENs) that fit this mold have been isolated.

Biochemical mechanisms of signal transduction can be gauged by the conservation of interacting protein folds in a pathway. Miklos and Rubin (1996) Cell 86:521-529; Chothia (1994) Develop. 1994 Suppl., 27-33. At present, the Toll signaling paradigm involves some molecules whose roles are narrowly defined by their structures, actions or fates: Pelle is a Ser/Thr kinase (phosphorylation), Dorsal is an NF- $\kappa$ B-like transcription factor (DNA-binding) and Cactus is an ankyrin-repeat inhibitor (Dorsal binding, degradation). Belvin and Anderson (1996) Ann. Rev. Cell Develop. Biol. 12:393-416. By contrast, the functions of the Toll TH domain and Tube remain enigmatic. Like other cytokine receptors (Heldin (1995) Cell 80:213-223), ligand-mediated dimerization of Toll appears to be the triggering event: free cysteines in the juxtamembrane region of Toll create constitutively active receptor pairs (Schneider, et al. (1991) Genes Develop. 5:797-807), and chimeric Torso-Toll receptors signal as dimers (Galindo, et al. (1995) Develop. 121:2209-2218); yet, severe truncations or wholesale loss of the Toll ectodomain results in promiscuous intracellular signaling (Norris and Manley (1995) Genes Develop. 9:358-369; and Winans and Hashimoto (1995) Molec. Biol. Cell 6:587-596), reminiscent of oncogenic receptors with catalytic domains (Heldin (1995) Cell 80:213-223). Tube is membrane-localized, engages the N-terminal (death) domain of Pelle and is phosphorylated, but neither Toll-Tube or Toll-Pelle interactions are registered by two-hybrid analysis (Galindo, et al. (1995) Develop. 121:2209-2218; and Großhans, et al. (1994) Nature 372:563-566); this latter result suggests that the conformational 'state' of the Toll TH domain somehow affects factor recruitment. Norris and Manley (1996) Genes Develop. 10:862-872; and Galindo, et al. (1995) Develop. 121:2209-2218.

At the heart of these vexing issues is the structural nature of the Toll TH module. To address this question, we have taken advantage of the evolutionary diversity of TH sequences from insects, plants and vertebrates, incorporating the human DTLR chains, and extracted the minimal, conserved protein core for structure prediction and fold recognition (Fig. 2). The strongly predicted ( $\beta/\alpha$ )<sub>5</sub> TH domain fold with its asymmetric cluster of acidic residues is topologically identical to the structures of response regulators in bacterial two-component signaling pathways (Volz (1993) Biochemistry 32:11741-11753; and Parkinson (1993) Cell 73:857-871) (Fig. 2). The prototype chemotaxis regulator CheY transiently binds a divalent cation in an 'aspartate pocket' at the C-end of the core  $\beta$ -sheet; this cation provides electrostatic stability and facilitates the activating phosphorylation of an invariant Asp. Volz (1993) Biochemistry 32:11741-11753. Likewise, the TH domain may capture cations in its acidic nest, but activation, and downstream signaling, could depend on the specific binding of a negatively charged moiety: anionic ligands can overcome intensely negative binding-site potentials by locking into precise hydrogen-bond networks. Ledvina, et al. (1996) Proc. Natl. Acad. Sci. USA 93:6786-6791. Intriguingly, the TH domain may not simply act as a passive scaffold for the assembly of a Tube/Pelle complex for Toll, or homologous systems in plants and vertebrates, but instead actively participate as a true conformational trigger in the signal transducing machinery. Perhaps explaining the conditional binding of a Tube/Pelle complex, Toll dimerization could promote unmasking, by regulatory receptor tails (Norris and Manley (1995) Genes Develop. 9:358-369; Norris and Manley (1996) Genes Develop. 10:862-872), or binding by small molecule activators of the TH pocket. However, 'free' TH modules inside the cell (Norris and Manley (1995) Genes Develop. 9:358-369;

Winans and Hashimoto (1995) Molec. Biol. Cell 6:587-596) could act as catalytic, CheY-like triggers by activating and docking with errant Tube/Pelle complexes.

5 Morphogenetic receptors and immune defense.

- The evolutionary link between insect and vertebrate immune systems is stamped in DNA: genes encoding antimicrobial factors in insects display upstream motifs similar to acute phase response elements known to bind
- 10 NF- $\kappa$ B transcription factors in mammals. Hultmark (1993) Trends Genet. 9:178-183. Dorsal, and two Dorsal-related factors, Dif and Relish, help induce these defense proteins after bacterial challenge (Reichhart, et al. (1993) C. R. Acad. Sci. Paris 316:1218-1224; Ip, et al. (1993) Cell 75:753-763; and Dushay, et al. (1996) Proc.
- 15 Natl. Acad. Sci. USA 93:10343-10347); Toll, or other DTLRs, likely modulate these rapid immune responses in adult *Drosophila* (Lemaitre, et al. (1996) Cell 86:973-983; and Rosetto, et al. (1995) Biochem. Biophys. Res.
- 20 Commun. 209:111-116). These mechanistic parallels to the IL-1 inflammatory response in vertebrates are evidence of the functional versatility of the Toll signaling pathway, and suggest an ancient synergy between embryonic patterning and innate immunity (Belvin and Anderson
- 25 (1996) Ann. Rev. Cell Develop. Biol. 12:393-416; Lemaitre, et al. (1996) Cell 86:973-983; Wasserman (1993) Molec. Biol. Cell 4:767-771; Wilson, et al. (1997) Curr. Biol. 7:175-178; Hultmark (1993) Trends Genet. 9:178-183; Reichhart, et al. (1993) C. R. Acad. Sci. Paris 316:1218-
- 30 1224; Ip, et al. (1993) Cell 75:753-763; Dushay, et al. (1996) Proc. Natl. Acad. Sci. USA 93:10343-10347; Rosetto, et al. (1995) Biochem. Biophys. Res. Commun. 209:111-116; Medzhitov and Janeway (1997) Curr. Opin. Immunol. 9:4-9; and Medzhitov and Janeway (1997) Curr.
- 35 Opin. Immunol. 9:4-9). The closer homology of insect and human DTLR proteins invites an even stronger overlap of biological functions that supersedes the purely immune

parallels to IL-1 systems, and lends potential molecular regulators to dorso-ventral and other transformations of vertebrate embryos. DeRobertis and Sasai (1996) Nature 380:37-40; and Arendt and Nübler-Jung (1997) Mech. Develop. 61:7-21.

The present description of an emergent, robust receptor family in humans mirrors the recent discovery of the vertebrate Frizzled receptors for Wnt patterning factors. Wang, et al. (1996) J. Biol. Chem. 271:4468-4476. As numerous other cytokine-receptor systems have roles in early development (Lemaire and Kodjabachian (1996) Trends Genet. 12:525-531), perhaps the distinct cellular contexts of compact embryos and gangly adults simply result in familiar signaling pathways and their diffusible triggers having different biological outcomes at different times, e.g., morphogenesis versus immune defense for DTLRs. For insect, plant, and human Toll-related systems (Hardiman, et al. (1996) Oncogene 13:2467-2475; Wilson, et al. (1997) Curr. Biol. 7:175-178), these signals course through a regulatory TH domain that intriguingly resembles a bacterial transducing engine (Parkinson (1993) Cell 73:857-871).

In particular, the DTLR6 exhibits structural features which establish its membership in the family. Moreover, members of the family have been implicated in a number of significant developmental disease conditions and with function of the innate immune system. In particular, the DTLR6 has been mapped to the X chromosome to a location which is a hot spot for major developmental abnormalities. See, e.g., The Sanger Center: human X chromosome website <http://www.sanger.ac.uk/HGP/ChrX/index.shtml>; and the Baylor College of Medicine Human Genome Sequencing website <http://gc.bcm.tmc.edu:8088/cgi-bin/seq/home>.

The accession number for the deposited PAC is AC003046. This accession number contains sequence from two PACs: RPC-164K3 and RPC-263P4. These two PAC



sequences mapped on human chromosome Xp22 at the Baylor web site between STS markers DXS704 and DXS7166. This region is a "hot spot" for severe developmental abnormalities.

5

### III. Amplification of DTLR fragment by PCR

Two appropriate primer sequences are selected (see Tables 1 through 10). RT-PCR is used on an appropriate mRNA sample selected for the presence of message to  
10 produce a partial or full length cDNA, e.g., a sample which expresses the gene. See, e.g., Innis, et al. (eds. 1990) PCR Protocols: A Guide to Methods and Applications Academic Press, San Diego, CA; and Dieffenbach and Dveksler (1995; eds.) PCR Primer: A Laboratory Manual  
15 Cold Spring Harbor Press, CSH, NY. Such will allow determination of a useful sequence to probe for a full length gene in a cDNA library. The TLR6 is a contiguous sequence in the genome, which may suggest that the other TLRs are also. Thus, PCR on genomic DNA may yield full  
20 length contiguous sequence, and chromosome walking methodology would then be applicable. Alternatively, sequence databases will contain sequence corresponding to portions of the described embodiments, or closely related forms, e.g., alternative splicing, etc. Expression  
25 cloning techniques also may be applied on cDNA libraries.

### IV. Tissue distribution of DTLRs

Message for each gene encoding these DTLRs has been detected. See Figures 5A-5F. Other cells and tissues  
30 will be assayed by appropriate technology, e.g., PCR, immunoassay, hybridization, or otherwise. Tissue and organ cDNA preparations are available, e.g., from Clontech, Mountain View, CA. Identification of sources of natural expression are useful, as described.

35 Southern Analysis: DNA (5 µg) from a primary amplified cDNA library is digested with appropriate restriction enzymes to release the inserts, run on a 1% agarose gel and

transferred to a nylon membrane (Schleicher and Schuell, Keene, NH).

Samples for human mRNA isolation would typically include, e.g.: peripheral blood mononuclear cells  
5 (monocytes, T cells, NK cells, granulocytes, B cells), resting (T100); peripheral blood mononuclear cells, activated with anti-CD3 for 2, 6, 12 h pooled (T101); T cell, TH0 clone Mot 72, resting (T102); T cell, TH0 clone Mot 72, activated with anti-CD28 and anti-CD3 for 3, 6,  
10 12 h pooled (T103); T cell, TH0 clone Mot 72, anergic treated with specific peptide for 2, 7, 12 h pooled (T104); T cell, TH1 clone HY06, resting (T107); T cell, TH1 clone HY06, activated with anti-CD28 and anti-CD3 for 3, 6, 12 h pooled (T108); T cell, TH1 clone HY06, anergic  
15 treated with specific peptide for 2, 6, 12 h pooled (T109); T cell, TH2 clone HY935, resting (T110); T cell, TH2 clone HY935, activated with anti-CD28 and anti-CD3 for 2, 7, 12 h pooled (T111); T cells CD4+CD45RO- T cells polarized 27 days in anti-CD28, IL-4, and anti IFN- $\gamma$ , TH2  
20 polarized, activated with anti-CD3 and anti-CD28 4 h (T116); T cell tumor lines Jurkat and Hut78, resting (T117); T cell clones, pooled AD130.2, Tc783.12, Tc783.13, Tc783.58, Tc782.69, resting (T118); T cell random  $\gamma\delta$  T cell clones, resting (T119); Splenocytes,  
25 resting (B100); Splenocytes, activated with anti-CD40 and IL-4 (B101); B cell EBV lines pooled WT49, RSE, JY, CVIR, 721.221, RM3, HSY, resting (B102); B cell line JY, activated with PMA and ionomycin for 1, 6 h pooled (B103); NK 20 clones pooled, resting (K100); NK 20 clones  
30 pooled, activated with PMA and ionomycin for 6 h (K101); NKL clone, derived from peripheral blood of LGL leukemia patient, IL-2 treated (K106); NK cytotoxic clone 640-A30-1, resting (K107); hematopoietic precursor line TFL1, activated with PMA and ionomycin for 1, 6 h pooled  
35 (C100); U937 premonocytic line, resting (M100); U937 premonocytic line, activated with PMA and ionomycin for 1, 6 h pooled (M101); elutriated monocytes, activated

with LPS, IFN $\gamma$ , anti-IL-10 for 1, 2, 6, 12, 24 h pooled (M102); elutriated monocytes, activated with LPS, IFN $\gamma$ , IL-10 for 1, 2, 6, 12, 24 h pooled (M103); elutriated monocytes, activated with LPS, IFN $\gamma$ , anti-IL-10 for 4, 16  
5 h pooled (M106); elutriated monocytes, activated with LPS, IFN $\gamma$ , IL-10 for 4, 16 h pooled (M107); elutriated monocytes, activated LPS for 1 h (M108); elutriated monocytes, activated LPS for 6 h (M109); DC 70% CD1a+, from CD34+ GM-CSF, TNF $\alpha$  12 days, resting (D101); DC 70%  
10 CD1a+, from CD34+ GM-CSF, TNF $\alpha$  12 days, activated with PMA and ionomycin for 1 hr (D102); DC 70% CD1a+, from CD34+ GM-CSF, TNF $\alpha$  12 days, activated with PMA and ionomycin for 6 hr (D103); DC 95% CD1a+, from CD34+ GM-CSF, TNF $\alpha$  12 days FACS sorted, activated with PMA and  
15 ionomycin for 1, 6 h pooled (D104); DC 95% CD14+, ex CD34+ GM-CSF, TNF $\alpha$  12 days FACS sorted, activated with PMA and ionomycin 1, 6 hr pooled (D105); DC CD1a+ CD86+, from CD34+ GM-CSF, TNF $\alpha$  12 days FACS sorted, activated with PMA and ionomycin for 1, 6 h pooled (D106); DC from  
20 monocytes GM-CSF, IL-4 5 days, resting (D107); DC from monocytes GM-CSF, IL-4 5 days, resting (D108); DC from monocytes GM-CSF, IL-4 5 days, activated LPS 4, 16 h pooled (D109); DC from monocytes GM-CSF, IL-4 5 days, activated TNF $\alpha$ , monocyte supe for 4, 16 h pooled (D110);  
25 leiomyoma L11 benign tumor (X101); normal myometrium M5 (O115); malignant leiomyosarcoma GS1 (X103); lung fibroblast sarcoma line MRC5, activated with PMA and ionomycin for 1, 6 h pooled (C101); kidney epithelial carcinoma cell line CHA, activated with PMA and ionomycin  
30 for 1, 6 h pooled (C102); kidney fetal 28 wk male (O100); lung fetal 28 wk male (O101); liver fetal 28 wk male (O102); heart fetal 28 wk male (O103); brain fetal 28 wk male (O104); gallbladder fetal 28 wk male (O106); small intestine fetal 28 wk male (O107); adipose tissue fetal  
35 28 wk male (O108); ovary fetal 25 wk female (O109); uterus fetal 25 wk female (O110); testes fetal 28 wk male

(O111); spleen fetal 28 wk male (O112); adult placenta 28 wk (O113); and tonsil inflamed, from 12 year old (X100).

- Samples for mouse mRNA isolation can include, e.g.:  
resting mouse fibroblastic L cell line (C200); Braf:ER  
5 (Braf fusion to estrogen receptor) transfected cells, control (C201); T cells, TH1 polarized (Mell4 bright, CD4+ cells from spleen, polarized for 7 days with IFN- $\gamma$  and anti IL-4; T200); T cells, TH2 polarized (Mell4 bright, CD4+ cells from spleen, polarized for 7 days with  
10 IL-4 and anti-IFN- $\gamma$ ; T201); T cells, highly TH1 polarized (see Openshaw, et al. (1995) J. Exp. Med. 182:1357-1367; activated with anti-CD3 for 2, 6, 16 h pooled; T202); T cells, highly TH2 polarized (see Openshaw, et al. (1995) J. Exp. Med. 182:1357-1367; activated with anti-CD3 for  
15 2, 6, 16 h pooled; T203); CD44- CD25+ pre T cells, sorted from thymus (T204); TH1 T cell clone D1.1, resting for 3 weeks after last stimulation with antigen (T205); TH1 T cell clone D1.1, 10  $\mu$ g/ml ConA stimulated 15 h (T206); TH2 T cell clone CDC35, resting for 3 weeks after last  
20 stimulation with antigen (T207); TH2 T cell clone CDC35, 10  $\mu$ g/ml ConA stimulated 15 h (T208); Mell4+ naive T cells from spleen, resting (T209); Mell4+ T cells, polarized to Th1 with IFN- $\gamma$ /IL-12/anti-IL-4 for 6, 12, 24 h pooled (T210); Mell4+ T cells, polarized to Th2 with  
25 IL-4/anti-IFN- $\gamma$  for 6, 13, 24 h pooled (T211); unstimulated mature B cell leukemia cell line A20 (B200); unstimulated B cell line CH12 (B201); unstimulated large B cells from spleen (B202); B cells from total spleen, LPS activated (B203); metrizamide enriched dendritic  
30 cells from spleen, resting (D200); dendritic cells from bone marrow, resting (D201); monocyte cell line RAW 264.7 activated with LPS 4 h (M200); bone-marrow macrophages derived with GM and M-CSF (M201); macrophage cell line J774, resting (M202); macrophage cell line J774 + LPS +  
35 anti-IL-10 at 0.5, 1, 3, 6, 12 h pooled (M203); macrophage cell line J774 + LPS + IL-10 at 0.5, 1, 3, 5, 12 h pooled (M204); aerosol challenged mouse lung tissue,

Th2 primers, aerosol OVA challenge 7, 14, 23 h pooled  
(see Garlisi, et al. (1995) Clinical Immunology and  
Immunopathology 75:75-83; X206); Nippostrongylus-infected  
lung tissue (see Coffman, et al. (1989) Science 245:308-  
5 310; X200); total adult lung, normal (O200); total lung,  
rag-1 (see Schwarz, et al. (1993) Immunodeficiency 4:249-  
252; O205); IL-10 K.O. spleen (see Kuhn, et al. (1991) Cell  
75:263-274; X201); total adult spleen, normal  
(O201); total spleen, rag-1 (O207); IL-10 K.O. Peyer's  
10 patches (O202); total Peyer's patches, normal (O210); IL-  
10 K.O. mesenteric lymph nodes (X203); total mesenteric  
lymph nodes, normal (O211); IL-10 K.O. colon (X203);  
total colon, normal (O212); NOD mouse pancreas (see  
Makino, et al. (1980) Jikken Dobutsu 29:1-13; X205);  
15 total thymus, rag-1 (O208); total kidney, rag-1 (O209);  
total heart, rag-1 (O202); total brain, rag-1 (O203);  
total testes, rag-1 (O204); total liver, rag-1 (O206);  
rat normal joint tissue (O300); and rat arthritic joint  
tissue (X300).

20

#### V. Cloning of species counterparts of DTLRs

Various strategies are used to obtain species  
counterparts of these DTLRs, preferably from other  
25 primates. One method is by cross hybridization using  
closely related species DNA probes. It may be useful to  
go into evolutionarily similar species as intermediate  
steps. Another method is by using specific PCR primers  
based on the identification of blocks of similarity or  
30 difference between particular species, e.g., human,  
genes, e.g., areas of highly conserved or nonconserved  
polypeptide or nucleotide sequence. Alternatively,  
antibodies may be used for expression cloning.

#### 35 VI. Production of mammalian DTLR protein

An appropriate, e.g., GST, fusion construct is  
engineered for expression, e.g., in *E. coli*. For

- example, a mouse IGIF pGex plasmid is constructed and transformed into *E. coli*. Freshly transformed cells are grown in LB medium containing 50 µg/ml ampicillin and induced with IPTG (Sigma, St. Louis, MO). After
- 5 overnight induction, the bacteria are harvested and the pellets containing the DTLR protein are isolated. The pellets are homogenized in TE buffer (50 mM Tris-base pH 8.0, 10 mM EDTA and 2 mM pefabloc) in 2 liters. This material is passed through a microfluidizer
- 10 (Microfluidics, Newton, MA) three times. The fluidized supernatant is spun down on a Sorvall GS-3 rotor for 1 h at 13,000 rpm. The resulting supernatant containing the DTLR protein is filtered and passed over a glutathione-SEPHAROSE column equilibrated in 50 mM Tris-base pH 8.0.
- 15 The fractions containing the DTLR-GST fusion protein are pooled and cleaved with thrombin (Enzyme Research Laboratories, Inc., South Bend, IN). The cleaved pool is then passed over a Q-SEPHAROSE column equilibrated in 50 mM Tris-base. Fractions containing DTLR are pooled and
- 20 diluted in cold distilled H<sub>2</sub>O, to lower the conductivity, and passed back over a fresh Q-Sepharose column, alone or in succession with an immunoaffinity antibody column.. Fractions containing the DTLR protein are pooled, aliquoted, and stored in the -70° C freezer.
- 25 Comparision of the CD spectrum with DTLR1 protein may suggest that the protein is correctly folded. See Hazuda, et al. (1969) J. Biol. Chem. 264:1689-1693.

#### VII. Biological Assays with DTLRs

- 30 Biological assays will generally be directed to the ligand binding feature of the protein or to the kinase/phosphatase activity of the receptor. The activity will typically be reversible, as are many other enzyme actions. mediate phosphatase or phosphorylase
- 35 activities, which activities are easily measured by standard procedures. See, e.g., Hardie, et al. (eds. 1995) The Protein Kinase FactBook vols. I and II,

- Academic Press, San Diego, CA; Hanks, et al. (1991) Meth. Enzymol. 200:38-62; Hunter, et al. (1992) Cell 70:375-388; Lewin (1990) Cell 61:743-752; Pines, et al. (1991) Cold Spring Harbor Symp. Quant. Biol. 56:449-463; and  
5 Parker, et al. (1993) Nature 363:736-738.

The family of interleukins 1 contains molecules, each of which is an important mediator of inflammatory disease. For a comprehensive review, see Dinarello (1996) "Biologic basis for interleukin-1 in disease"  
10 Blood 87:2095-2147. There are suggestions that the various Toll ligands may play important roles in the initiation of disease, particularly inflammatory responses. The finding of novel proteins related to the IL-1 family furthers the identification of molecules that  
15 provide the molecular basis for initiation of disease and allow for the development of therapeutic strategies of increased range and efficacy.

VIII. Preparation of antibodies specific for, e.g.,  
20 DTLR4

Inbred Balb/c mice are immunized intraperitoneally with recombinant forms of the protein, e.g., purified DTLR4 or stable transfected NIH-3T3 cells. Animals are boosted at appropriate time points with protein, with or  
25 without additional adjuvant, to further stimulate antibody production. Serum is collected, or hybridomas produced with harvested spleens.

Alternatively, Balb/c mice are immunized with cells transformed with the gene or fragments thereof, either  
30 endogenous or exogenous cells, or with isolated membranes enriched for expression of the antigen. Serum is collected at the appropriate time, typically after numerous further administrations. Various gene therapy techniques may be useful, e.g., in producing protein in  
35 situ, for generating an immune response.

Monoclonal antibodies may be made. For example, splenocytes are fused with an appropriate fusion partner

and hybridomas are selected in growth medium by standard procedures. Hybridoma supernatants are screened for the presence of antibodies which bind to the desired DTLR, e.g., by ELISA or other assay. Antibodies which  
5 specifically recognize specific DTLR embodiments may also be selected or prepared.

In another method, synthetic peptides or purified protein are presented to an immune system to generate monoclonal or polyclonal antibodies. See, e.g., Coligan  
10 (1991) Current Protocols in Immunology Wiley/Greene; and Harlow and Lane (1989) Antibodies: A Laboratory Manual Cold Spring Harbor Press. In appropriate situations, the binding reagent is either labeled as described above, e.g., fluorescence or otherwise, or immobilized to a  
15 substrate for panning methods. Nucleic acids may also be introduced into cells in an animal to produce the antigen, which serves to elicit an immune response. See, e.g., Wang, et al. (1993) Proc. Nat'l. Acad. Sci. 90:4156-4160; Barry, et al. (1994) BioTechniques 16:616-  
20 619; and Xiang, et al. (1995) Immunity 2: 129-135.

#### IX. Production of fusion proteins with, e.g., DTLR5

Various fusion constructs are made with DTLR5. This portion of the gene is fused to an epitope tag, e.g., a  
25 FLAG tag, or to a two hybrid system construct. See, e.g., Fields and Song (1989) Nature 340:245-246.

The epitope tag may be used in an expression cloning procedure with detection with anti-FLAG antibodies to detect a binding partner, e.g., ligand for the respective  
30 DTLR5. The two hybrid system may also be used to isolate proteins which specifically bind to DTLR5.

#### X. Chromosomal mapping of DTLRs

Chromosome spreads are prepared. In situ  
35 hybridization is performed on chromosome preparations obtained from phytohemagglutinin-stimulated lymphocytes cultured for 72 h. 5-bromodeoxyuridine is added for the



final seven hours of culture (60 µg/ml of medium), to ensure a posthybridization chromosomal banding of good quality.

An appropriate fragment, e.g., a PCR fragment, amplified with the help of primers on total B cell cDNA template, is cloned into an appropriate vector. The vector is labeled by nick-translation with <sup>3</sup>H. The radiolabeled probe is hybridized to metaphase spreads as described in Mattei, et al. (1985) Hum. Genet. 69:327-331.

After coating with nuclear track emulsion (KODAK NTB<sub>2</sub>), slides are exposed, e.g., for 18 days at 4° C. To avoid any slipping of silver grains during the banding procedure, chromosome spreads are first stained with buffered Giemsa solution and metaphase photographed. R-banding is then performed by the fluorochrome-photolysis-Giemsa (FPG) method and metaphases rephotographed before analysis.

Alternatively, FISH can be performed, as described above. The DTLR genes are located on different chromosomes. DTLR2 and DTLR3 are localized to human chromosome 4; DTLR4 is localized to human chromosome 9, and DTLR5 is localized to human chromosome 1. See Figures 4A-4D.

#### XI. Structure activity relationship

Information on the criticality of particular residues is determined using standard procedures and analysis. Standard mutagenesis analysis is performed, e.g., by generating many different variants at determined positions, e.g., at the positions identified above, and evaluating biological activities of the variants. This may be performed to the extent of determining positions which modify activity, or to focus on specific positions to determine the residues which can be substituted to either retain, block, or modulate biological activity.

Alternatively, analysis of natural variants can indicate what positions tolerate natural mutations. This may result from populational analysis of variation among individuals, or across strains or species. Samples from  
5 selected individuals are analysed, e.g., by PCR analysis and sequencing. This allows evaluation of population polymorphisms.

#### XI. Isolation of a ligand for a DTLR

10 A DTLR can be used as a specific binding reagent to identify its binding partner, by taking advantage of its specificity of binding, much like an antibody would be used. A binding reagent is either labeled as described above, e.g., fluorescence or otherwise, or immobilized to  
15 a substrate for panning methods.

The binding composition is used to screen an expression library made from a cell line which expresses a binding partner, i.e., ligand, preferably membrane associated. Standard staining techniques are used to  
20 detect or sort surface expressed ligand, or surface expressing transformed cells are screened by panning. Screening of intracellular expression is performed by various staining or immunofluorescence procedures. See also McMahan, et al. (1991) EMBO J. 10:2821-2832.

25 For example, on day 0, precoat 2-chamber permanox slides with 1 ml per chamber of fibronectin, 10 ng/ml in PBS, for 30 min at room temperature. Rinse once with PBS. Then plate COS cells at  $2-3 \times 10^5$  cells per chamber in 1.5 ml of growth media. Incubate overnight at 37' C.

30 On day 1 for each sample, prepare 0.5 ml of a solution of 66  $\mu$ g/ml DEAE-dextran, 66  $\mu$ M chloroquine, and 4  $\mu$ g DNA in serum free DME. For each set, a positive control is prepared, e.g., of DTLR-FLAG cDNA at 1 and 1/200 dilution, and a negative mock. Rinse cells with  
35 serum free DME. Add the DNA solution and incubate 5 hr at 37' C. Remove the medium and add 0.5 ml 10% DMSO in

DME for 2.5 min. Remove and wash once with DME. Add 1.5 ml growth medium and incubate overnight.

On day 2, change the medium. On days 3 or 4, the cells are fixed and stained. Rinse the cells twice with  
5 Hank's Buffered Saline Solution (HBSS) and fix in 4% paraformaldehyde (PFA)/glucose for 5 min. Wash 3X with HBSS. The slides may be stored at -80° C after all liquid is removed. For each chamber, 0.5 ml incubations are performed as follows. Add HBSS/saponin (0.1%) with  
10 32 µl/ml of 1 M NaN<sub>3</sub> for 20 min. Cells are then washed with HBSS/saponin 1X. Add appropriate DTLR or DTLR/antibody complex to cells and incubate for 30 min. Wash cells twice with HBSS/saponin. If appropriate, add first antibody for 30 min. Add second antibody, e.g.,  
15 Vector anti-mouse antibody, at 1/200 dilution, and incubate for 30 min. Prepare ELISA solution, e.g., Vector Elite ABC horseradish peroxidase solution, and preincubate for 30 min. Use, e.g., 1 drop of solution A (avidin) and 1 drop solution B (biotin) per 2.5 ml  
20 HBSS/saponin. Wash cells twice with HBSS/saponin. Add ABC HRP solution and incubate for 30 min. Wash cells twice with HBSS, second wash for 2 min, which closes cells. Then add Vector diaminobenzoic acid (DAB) for 5 to 10 min. Use 2 drops of buffer plus 4 drops DAB plus 2  
25 drops of H<sub>2</sub>O<sub>2</sub> per 5 ml of glass distilled water. Carefully remove chamber and rinse slide in water. Air dry for a few minutes, then add 1 drop of Crystal Mount and a cover slip. Bake for 5 min at 85-90° C.

Evaluate positive staining of pools and  
30 progressively subclone to isolation of single genes responsible for the binding.

Alternatively, DTLR reagents are used to affinity purify or sort out cells expressing a putative ligand. See, e.g., Sambrook, et al. or Ausubel, et al.

35 Another strategy is to screen for a membrane bound receptor by panning. The receptor cDNA is constructed as described above. The ligand can be immobilized and used

to immobilize expressing cells. Immobilization may be achieved by use of appropriate antibodies which recognize, e.g., a FLAG sequence of a DTLR fusion construct, or by use of antibodies raised against the first antibodies. Recursive cycles of selection and amplification lead to enrichment of appropriate clones and eventual isolation of receptor expressing clones.

Phage expression libraries can be screened by mammalian DTLRs. Appropriate label techniques, e.g., anti-FLAG antibodies, will allow specific labeling of appropriate clones.

All citations herein are incorporated herein by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Many modifications and variations of this invention can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. The specific embodiments described herein are offered by way of example only, and the invention is to be limited by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled; and the invention is not to be limited by the specific embodiments that have been presented herein by way of example.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: (A) NAME: Schering Corporation  
(B) STREET: 2000 Galloping Hill Road  
(C) CITY: Kenilworth  
10 (D) STATE: New Jersey  
(E) COUNTRY: USA  
(F) POSTAL CODE: 07033  
(G) TELEPHONE: (908) 298-4000  
(H) TELEFAX: (908) 298-5388
- 15 (ii) TITLE OF INVENTION: HUMAN RECEPTOR PROTEINS; RELATED  
REAGENTS AND METHODS
- (iii) NUMBER OF SEQUENCES: 35
- 20 (iv) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Macintosh Power PC  
(C) OPERATING SYSTEM: 8.0  
25 (D) SOFTWARE: Microsoft Word 6.0
- (v) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
30 (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:  
(A) APPLICATION NO.: USSN 60/044,293  
(B) FILING DATE: 07-MAY-1997
- 35 (A) APPLICATION NO.: USSN 60/072,212  
(B) FILING DATE: 22-JAN-1998
- (A) APPLICATION NO.: USSN 60/076,947  
(B) FILING DATE: 05-MAR-1998
- 40 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2367 base pairs  
45 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 50 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..2358
- 55 (ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 67..2358

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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30	ATC CAG TAT CTT GAT ATC AGT GTT TTC AAA TTC AAC CAG GAA TTG GAA Ile Gln Tyr Leu Asp Ile Ser Val Phe Lys Phe Asn Gln Glu Leu Glu 60 65 70	288
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50	GGG TTG AGC ACC ACA CAC TTA GAA AAA TCT AGT GTG CTG CCA ATT GCT Gly Leu Ser Thr Thr His Leu Glu Lys Ser Ser Val Leu Pro Ile Ala 125 130 135	480
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65	CAC ATT GTG TTC CCC ACA AAC AAA GAA TTC CAT TTT ATT TTG GAT GTG His Ile Val Phe Pro Thr Asn Lys Glu Phe His Phe Ile Leu Asp Val 175 180 185	624
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75	CTA GAA GAT AAC AAA TGT TCT TAC TTC CTA AGT ATT CTG GCG AAA CTT Leu Glu Asp Asn Lys Cys Ser Tyr Phe Leu Ser Ile Leu Ala Lys Leu	720

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20	CAC CAA GTT GTC AGC GAT GTG TTC GGT TTT CCG CAA AGT TAT ATC TAT His Gln Val Val Ser Asp Val Phe Gly Phe Pro Gln Ser Tyr Ile Tyr	285	290	295
25	GAA ATC TTT TCG AAT ATG AAC ATC AAA AAT TTC ACA GTG TCT GGT ACA Glu Ile Phe Ser Asn Met Asn Ile Lys Asn Phe Thr Val Ser Gly Thr	300	305	310
30	CGC ATG GTC CAC ATG CTT TGC CCA TCC AAA ATT AGC CCG TTC CTG CAT Arg Met Val His Met Leu Cys Pro Ser Lys Ile Ser Pro Phe Leu His	315	320	325
	TTG GAT TTT TCC AAT AAT CTC TTA ACA GAC ACG GTT TTT GAA AAT TGT Leu Asp Phe Ser Asn Asn Leu Leu Thr Asp Thr Val Phe Glu Asn Cys	335	340	345
35	GGG CAC CTT ACT GAG TTG GAG ACA CTT ATT TTA CAA ATG AAT CAA TTA Gly His Leu Thr Glu Leu Glu Thr Leu Ile Leu Gln Met Asn Gln Leu	350	355	360
40	AAA GAA CTT TCA AAA ATA GCT GAA ATG ACT ACA CAG ATG AAG TCT CTG Lys Glu Leu Ser Lys Ile Ala Glu Met Thr Thr Gln Met Lys Ser Leu	365	370	375
45	CAA CAA TTG GAT ATT AGC CAG AAT TCT GTA AGC TAT GAT GAA AAG AAA Gln Gln Leu Asp Ile Ser Gln Asn Ser Val Ser Tyr Asp Glu Lys Lys	380	385	390
50	GGA GAC TGT TCT TGG ACT AAA AGT TTA TTA AGT TTA AAT ATG TCT TCA Gly Asp Cys Ser Trp Thr Lys Ser Leu Leu Ser Leu Asn Met Ser Ser	395	400	405
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40	AAC ATA CCC TTA GAA GAA CTC CAA AGA AAT CTC CAG TTT CAT GCA TTT Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe His Ala Phe 605 610 615	1920
45	ATT TCA TAT AGT GGG CAC GAT TCT TTC TGG GTG AAG AAT GAA TTA TTG Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn Glu Leu Leu 620 625 630	1968
	CCA AAC CTA GAG AAA GAA GGT ATG CAG ATT TGC CTT CAT GAG AGA AAC Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His Glu Arg Asn 635 640 645 650	2016
50	TTT GTT CCT GGC AAG AGC ATT GTG GAA AAT ATC ATC ACC TGC ATT GAG Phe Val Pro Gly Lys Ser Ile Val Leu Glu Asn Ile Ile Thr Cys Ile Glu 655 660 665	2064
55	AAG AGT TAC AAG TCC ATC TTT GTT TTG TCT CCC AAC TTT GTC CAG AGT Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser 670 675 680	2112
60	GAA TGG TGC CAT TAT GAA CTC TAC TTT GCC CAT CAC AAT CTC TTT CAT Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His 685 690 695	2160



	GAA GGA TCT AAT AGC TTA ATC CTG ATC TTG CTG GAA CCC ATT CCG CAG	2208
	Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln	
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5	TAC TCC ATT CCT AGC AGT TAT CAC AAG CTC AAA AGT CTC ATG GCC AGG	2256
	Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu Met Ala Arg	
	715 720 725	
10	AGG ACT TAT TTG GAA TGG CCC AAG GAA AAG AGC AAA CGT GGC CTT TTT	2304
	Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe	
	735 740 745	
15	TGG GCT AAC TTA AGG GCA GCC ATT AAT ATT AAG CTG ACA GAG CAA GCA	2352
	Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr Glu Gln Ala	
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	Lys Lys	
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	(2) INFORMATION FOR SEQ ID NO:2:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 786 amino acids	
	(B) TYPE: amino acid	
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	(ii) MOLECULE TYPE: protein	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
	Met Thr Ser Ile Phe His Phe Ala Ile Ile Phe Met Leu Ile Leu Gln	
35	-22 -20 -15 -10	
	Ile Arg Ile Gln Leu Ser Glu Glu Ser Glu Phe Leu Val Asp Arg Ser	
	-5 1 5 10	
40	Lys Asn Gly Leu Ile His Val Pro Lys Asp Leu Ser Gln Lys Thr Thr	
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	30 35 40	
45	Ile Leu Ser Leu Ser Lys Leu Arg Ile Leu Ile Ile Ser His Asn Arg	
	45 50 55	
	Ile Gln Tyr Leu Asp Ile Ser Val Phe Lys Phe Asn Gln Glu Leu Glu	
50	60 65 70	
	Tyr Leu Asp Leu Ser His Asn Lys Leu Val Lys Ile Ser Cys His Pro	
	75 80 85 90	
55	Thr Val Asn Leu Lys His Leu Asp Leu Ser Phe Asn Ala Phe Asp Ala	
	95 100 105	
	Leu Pro Ile Cys Lys Glu Phe Gly Asn Met Ser Gln Leu Lys Phe Leu	
	110 115 120	
60	Gly Leu Ser Thr Thr His Leu Glu Lys Ser Ser Val Leu Pro Ile Ala	
	125 130 135	

His Leu Asn Ile Ser Lys Val Leu Leu Val Leu Gly Glu Thr Tyr Gly  
 140 145 150  
 5 Glu Lys Glu Asp Pro Glu Gly Leu Gln Asp Phe Asn Thr Glu Ser Leu  
 155 160 165 170  
 His Ile Val Phe Pro Thr Asn Lys Glu Phe His Phe Ile Leu Asp Val  
 175 180 185  
 10 Ser Val Lys Thr Val Ala Asn Leu Glu Leu Ser Asn Ile Lys Cys Val  
 190 195 200  
 15 Leu Glu Asp Asn Lys Cys Ser Tyr Phe Leu Ser Ile Leu Ala Lys Leu  
 205 210 215  
 Gln Thr Asn Pro Lys Leu Ser Ser Leu Thr Leu Asn Asn Ile Glu Thr  
 220 225 230  
 20 Thr Trp Asn Ser Phe Ile Arg Ile Leu Gln Leu Val Trp His Thr Thr  
 235 240 245 250  
 Val Trp Tyr Phe Ser Ile Ser Asn Val Lys Leu Gln Gly Gln Leu Asp  
 255 260 265  
 25 Phe Arg Asp Phe Asp Tyr Ser Gly Thr Ser Leu Lys Ala Leu Ser Ile  
 270 275 280  
 30 His Gln Val Val Ser Asp Val Phe Gly Phe Pro Gln Ser Tyr Ile Tyr  
 285 290 295  
 Glu Ile Phe Ser Asn Met Asn Ile Lys Asn Phe Thr Val Ser Gly Thr  
 300 305 310  
 35 Arg Met Val His Met Leu Cys Pro Ser Lys Ile Ser Pro Phe Leu His  
 315 320 325 330  
 Leu Asp Phe Ser Asn Asn Leu Leu Thr Asp Thr Val Phe Glu Asn Cys  
 335 340 345  
 40 Gly His Leu Thr Glu Leu Glu Thr Leu Ile Leu Gln Met Asn Gln Leu  
 350 355 360  
 45 Lys Glu Leu Ser Lys Ile Ala Glu Met Thr Thr Gln Met Lys Ser Leu  
 365 370 375  
 Gln Gln Leu Asp Ile Ser Gln Asn Ser Val Ser Tyr Asp Glu Lys Lys  
 380 385 390  
 50 Gly Asp Cys Ser Trp Thr Lys Ser Leu Leu Ser Leu Asn Met Ser Ser  
 395 400 405 410  
 Asn Ile Leu Thr Asp Thr Ile Phe Arg Cys Leu Pro Pro Arg Ile Lys  
 415 420 425  
 55 Val Leu Asp Leu His Ser Asn Lys Ile Lys Ser Ile Pro Lys Gln Val  
 430 435 440  
 Val Lys Leu Glu Ala Leu Gln Glu Leu Asn Val Ala Phe Asn Ser Leu  
 445 450 455

Thr Asp Leu Pro Gly Cys Gly Ser Phe Ser Ser Leu Ser Val Leu Ile  
 460 465 470  
 5 Ile Asp His Asn Ser Val Ser His Pro Ser Ala Asp Phe Phe Gln Ser  
 475 480 485 490  
 Cys Gln Lys Met Arg Ser Ile Lys Ala Gly Asp Asn Pro Phe Gln Cys  
 495 500 505  
 10 Thr Cys Glu Leu Gly Glu Phe Val Lys Asn Ile Asp Gln Val Ser Ser  
 510 515 520  
 Glu Val Leu Glu Gly Trp Pro Asp Ser Tyr Lys Cys Asp Tyr Pro Glu  
 525 530 535  
 15 Ser Tyr Arg Gly Thr Leu Leu Lys Asp Phe His Met Ser Glu Leu Ser  
 540 545 550  
 Cys Asn Ile Thr Leu Leu Ile Val Thr Ile Val Ala Thr Met Leu Val  
 555 560 565 570  
 20 Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr Leu Asp Leu Pro Trp  
 575 580 585  
 25 Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg Arg Ala Arg  
 590 595 600  
 Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe His Ala Phe  
 605 610 615  
 30 Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn Glu Leu Leu  
 620 625 630  
 35 Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His Glu Arg Asn  
 635 640 645 650  
 Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr Cys Ile Glu  
 655 660 665  
 40 Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser  
 670 675 680  
 Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His  
 685 690 695  
 45 Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln  
 700 705 710  
 Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu Met Ala Arg  
 715 720 725 730  
 50 Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe  
 735 740 745  
 55 Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr Glu Gln Ala  
 750 755 760  
 Lys Lys

60

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2355 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2352

(ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 67..2352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG CCA CAT ACT TTG TGG ATG GTG TGG GTC TTG GGG GTC ATC ATC AGC	48
Met Pro His Thr Leu Trp Met Val Trp Val Leu Gly Val Ile Ile Ser	
-22 -20 -15 -10	
CTC TCC AAG GAA GAA TCC TCC AAT CAG GCT TCT CTG TCT TGT GAC CGC	96
Leu Ser Lys Glu Glu Ser Ser Asn Gln Ala Ser Leu Ser Cys Asp Arg	
-5 1 5 10	
AAT GGT ATC TGC AAG GGC AGC TCA GGA TCT TTA AAC TCC ATT CCC TCA	144
Asn Gly Ile Cys Lys Gly Ser Ser Gly Ser Leu Asn Ser Ile Pro Ser	
15 20 25	
GGG CTC ACA GAA GCT GTA AAA AGC CTT GAC CTG TCC AAC AAC AGG ATC	192
Gly Leu Thr Glu Ala Val Lys Ser Leu Asp Leu Ser Asn Asn Arg Ile	
30 35 40	
ACC TAC ATT AGC AAC AGT GAC CTA CAG AGG TGT GTG AAC CTC CAG GCT	240
Thr Tyr Ile Ser Asn Ser Asp Leu Gln Arg Cys Val Asn Leu Gln Ala	
45 50 55	
CTG GTG CTG ACA TCC AAT GGA ATT AAC ACA ATA GAG GAA GAT TCT TTT	288
Leu Val Leu Thr Ser Asn Gly Ile Asn Thr Ile Glu Glu Asp Ser Phe	
60 65 70	
TCT TCC CTG GGC AGT CTT GAA CAT TTA GAC TTA TCC TAT AAT TAC TTA	336
Ser Ser Leu Gly Ser Leu Glu His Leu Asp Leu Ser Tyr Asn Tyr Leu	
75 80 85 90	
TCT AAT TTA TCG TCT TCC TGG TTC AAG CCC CTT TCT TCT TTA ACA TTC	384
Ser Asn Leu Ser Ser Ser Trp Phe Lys Pro Leu Ser Ser Leu Thr Phe	
95 100 105	
TTA AAC TTA CTG GGA AAT CCT TAC AAA ACC CTA GGG GAA ACA TCT CTT	432
Leu Asn Leu Leu Gly Asn Pro Tyr Lys Thr Leu Gly Glu Thr Ser Leu	
110 115 120	
TTT TCT CAT CTC ACA AAA TTG CAA ATC CTG AGA GTG GGA AAT ATG GAC	480
Phe Ser His Leu Thr Lys Leu Gln Ile Leu Arg Val Gly Asn Met Asp	
125 130 135	

	ACC TTC ACT AAG ATT CAA AGA AAA GAT TTT GCT GGA CTT ACC TTC CTT	528
	Thr Phe Thr Lys Ile Gln Arg Lys Asp Phe Ala Gly Leu Thr Phe Leu	
	140 145 150	
5	GAG GAA CTT GAG ATT GAT GCT TCA GAT CTA CAG AGC TAT GAG CCA AAA	576
	Glu Glu Leu Glu Ile Asp Ala Ser Asp Leu Gln Ser Tyr Glu Pro Lys	
	155 160 165 170	
10	AGT TTG AAG TCA ATT CAG AAC GTA AGT CAT CTG ATC CTT CAT ATG AAG	624
	Ser Leu Lys Ser Ile Gln Asn Val Ser His Leu Ile Leu His Met Lys	
	175 180 185	
15	CAG CAT ATT TTA CTG CTG GAG ATT TTT GTA GAT GTT ACA AGT TCC GTG	672
	Gln His Ile Leu Leu Leu Glu Ile Phe Val Asp Val Thr Ser Ser Val	
	190 195 200	
20	GAA TGT TTG GAA CTG CGA GAT ACT GAT TTG GAC ACT TTC CAT TTT TCA	720
	Glu Cys Leu Glu Leu Arg Asp Thr Asp Leu Asp Thr Phe His Phe Ser	
	205 210 215	
25	GAA CTA TCC ACT GGT GAA ACA AAT TCA TTG ATT AAA AAG TTT ACA TTT	768
	Glu Leu Ser Thr Gly Glu Thr Asn Ser Leu Ile Lys Phe Thr Phe	
	220 225 230	
30	AGA AAT GTG AAA ATC ACC GAT GAA AGT TTG TTT CAG GTT ATG AAA CTT	816
	Arg Asn Val Lys Ile Thr Asp Glu Ser Leu Phe Gln Val Met Lys Leu	
	235 240 245 250	
35	TTG AAT CAG ATT TCT GGA TTG TTA GAA TTA GAG TTT GAT GAC TGT ACC	864
	Leu Asn Gln Ile Ser Gly Leu Leu Glu Leu Glu Phe Asp Asp Cys Thr	
	255 260 265	
40	CTT AAT GGA GTT GGT AAT TTT AGA GCA TCT GAT AAT GAC AGA GTT ATA	912
	Leu Asn Gly Val Gly Asn Phe Arg Ala Ser Asp Asn Asp Arg Val Ile	
	270 275 280	
45	GAT CCA GGT AAA GTG GAA ACG TTA ACA ATC CGG AGG CTG CAT ATT CCA	960
	Asp Pro Gly Lys Val Glu Thr Leu Thr Ile Arg Arg Leu His Ile Pro	
	285 290 295	
50	AGG TTT TAC TTA TTT TAT GAT CTG AGC ACT TTA TAT TCA CTT ACA GAA	1008
	Arg Phe Tyr Leu Phe Tyr Asp Leu Ser Thr Leu Tyr Ser Leu Thr Glu	
	300 305 310	
55	AGA GTT AAA AGA ATC ACA GTA GAA AAC AGT AAA GTT TTT CTG GTT CCT	1056
	Arg Val Lys Arg Ile Thr Val Glu Asn Ser Lys Val Phe Leu Val Pro	
	315 320 325 330	
60	TGT TTA CTT TCA CAA CAT TTA AAA TCA TTA GAA TAC TTG GAT CTC AGT	1104
	Cys Leu Leu Ser Gln His Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser	
	335 340 345	
65	GAA AAT TTG ATG GTT GAA GAA TAC TTG AAA AAT TCA GCC TGT GAG GAT	1152
	Glu Asn Leu Met Val Glu Glu Tyr Leu Lys Asn Ser Ala Cys Glu Asp	
	350 355 360	
70	GCC TGG CCC TCT CTA CAA ACT TTA ATT TTA AGG CAA AAT CAT TTG GCA	1200
	Ala Trp Pro Ser Leu Gln Thr Leu Ile Leu Arg Gln Asn His Leu Ala	
	365 370 375	
75	TCA TTG GAA AAA ACC GGA GAG ACT TTG CTC ACT CTG AAA AAC TTG ACT	1248

	Ser	Leu	Glu	Lys	Thr	Gly	Glu	Thr	Leu	Leu	Thr	Leu	Lys	Asn	Leu	Thr	
	380						385					390					
5	AAC	ATT	GAT	ATC	AGT	AAG	AAT	AGT	TTT	CAT	TCT	ATG	CCT	GAA	ACT	TGT	1296
	Asn	Ile	Asp	Ile	Ser	Lys	Asn	Ser	Phe	His	Ser	Met	Pro	Glu	Thr	Cys	
	395					400					405				410		
10	CAG	TGG	CCA	GAA	AAG	ATG	AAA	TAT	TTG	AAC	TTA	TCC	AGC	ACA	CGA	ATA	1344
	Gln	Trp	Pro	Glu	Lys	Met	Lys	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Arg	Ile	
				415					420						425		
15	CAC	AGT	GTA	ACA	GGC	TGC	ATT	CCC	AAG	ACA	CTG	GAA	ATT	TTA	GAT	GTT	1392
	His	Ser	Val	Thr	Gly	Cys	Ile	Pro	Lys	Thr	Leu	Glu	Ile	Leu	Asp	Val	
				430					435					440			
20	AGC	AAC	AAC	AAT	CTC	AAT	TTA	TTT	TCT	TTG	AAT	TTG	CCG	CAA	CTC	AAA	1440
	Ser	Asn	Asn	Asn	Leu	Asn	Leu	Phe	Ser	Leu	Asn	Leu	Pro	Gln	Leu	Lys	
				445				450					455				
25	GAA	CTT	TAT	ATT	TCC	AGA	AAT	AAG	TTG	ATG	ACT	CTA	CCA	GAT	GCC	TCC	1488
	Glu	Leu	Tyr	Ile	Ser	Arg	Asn	Lys	Leu	Met	Thr	Leu	Pro	Asp	Ala	Ser	
				460				465				470					
30	CTC	TTA	CCC	ATG	TTA	CTA	TTG	AAA	ATC	AGT	AGG	AAT	GCA	ATA	ACT		1536
	Leu	Leu	Pro	Met	Leu	Leu	Val	Leu	Lys	Ile	Ser	Arg	Asn	Ala	Ile	Thr	
	475					480				485					490		
35	ACG	TTT	TCT	AAG	GAG	CAA	CTT	GAC	TCA	TTT	CAC	ACA	CTG	AAG	ACT	TTG	1584
	Thr	Phe	Ser	Lys	Glu	Gln	Leu	Asp	Ser	Phe	His	Thr	Leu	Lys	Thr	Leu	
				495						500					505		
40	GAA	GCT	GGT	GGC	AAT	AAC	TTC	ATT	TGC	TCC	TGT	GAA	TTC	CTC	TCC	TTC	1632
	Glu	Ala	Gly	Gly	Asn	Asn	Phe	Ile	Cys	Ser	Cys	Glu	Phe	Leu	Ser	Phe	
				510				515						520			
45	ACT	CAG	GAG	CAG	CAA	GCA	CTG	GCC	AAA	GTC	TTG	ATT	GAT	TGG	CCA	GCA	1680
	Thr	Gln	Glu	Gln	Gln	Ala	Leu	Ala	Lys	Val	Leu	Ile	Asp	Trp	Pro	Ala	
				525				530					535				
50	AAT	TAC	CTG	TGT	GAC	TCT	CCA	TCC	CAT	GTG	CGT	GGC	CAG	CAG	GTT	CAG	1728
	Asn	Tyr	Leu	Cys	Asp	Ser	Pro	Ser	His	Val	Arg	Gly	Gln	Gln	Val	Gln	
				540			545					550					
55	GAT	GTC	CGC	CTC	TCG	GTG	TCG	GAA	TGT	CAC	AGG	ACA	GCA	CTG	GTG	TCT	1776
	Asp	Val	Arg	Leu	Ser	Val	Ser	Glu	Cys	His	Arg	Thr	Ala	Leu	Val	Ser	
				555			560				565				570		
60	GGC	ATG	TGC	TGT	GCT	CTG	TTC	CTG	ATC	CTG	CTC	ACG	GGG	GTC	CTG		1824
	Gly	Met	Cys	Cys	Ala	Leu	Phe	Leu	Leu	Ile	Leu	Leu	Thr	Gly	Val	Leu	
				575					580					585			
65	TGC	CAC	CGT	TTC	CAT	GGC	CTG	TGG	TAT	ATG	AAA	ATG	ATG	TGG	GCC	TGG	1872
	Cys	His	Arg	Phe	His	Gly	Leu	Trp	Tyr	Met	Lys	Met	Met	Trp	Ala	Trp	
				590					595					600			
70	CTC	CAG	GCC	AAA	AGG	AAG	CCC	AGG	AAA	GCT	CCC	AGC	AGG	AAC	ATC	TGC	1920
	Leu	Gln	Ala	Lys	Arg	Lys	Pro	Arg	Lys	Ala	Pro	Ser	Arg	Asn	Ile	Cys	
				605				610					615				
75	TAT	GAT	GCA	TTT	GTT	TCT	TAC	AGT	GAG	CGG	GAT	GCC	TAC	TGG	GTG	GAG	1968
	Tyr	Asp	Ala	Phe	Val	Ser	Tyr	Ser	Glu	Arg	Asp	Ala	Tyr	Trp	Val	Glu	

	620	625	630	
5	AAC CTT ATG GTC CAG GAG CTG GAG AAC TTC AAT CCC CCC TTC AAG TTG Asn Leu Met Val Gln Glu Leu Asn Phe Asn Pro Pro Phe Lys Leu 635 640 645 650			2016
	TGT CTT CAT AAG CGG GAC TTC ATT CCT GGC AAG TGG ATC ATT GAC AAT Cys Leu His Lys Arg Asp Phe Ile Pro Gly Lys Trp Ile Ile Asp Asn 655 660 665			2064
10	ATC ATT GAC TCC ATT GAA AAG AGC CAC AAA ACT GTC TTT GTG CTT TCT Ile Ile Asp Ser Ile Glu Lys Ser His Lys Thr Val Phe Val Leu Ser 670 675 680			2112
15	GAA AAC TTT GTG AAG AGT GAG TGG TGC AAG TAT GAA CTG GAC TTC TCC Glu Asn Phe Val Lys Ser Glu Trp Cys Lys Tyr Glu Leu Asp Phe Ser 685 690 695			2160
20	CAT TTC CGT CTT TTT GAA GAG AAC AAT GAT GCT GCC ATT CTC ATT CTT His Phe Arg Leu Phe Glu Asn Asn Asp Ala Ala Ile Leu Ile Leu 700 705 710			2208
25	CTG GAG CCC ATT GAG AAA AAA GCC ATT CCC CAG CGC TTC TGC AAG CTG Leu Glu Pro Ile Glu Lys Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu 715 720 725 730			2256
	CGG AAG ATA ATG AAC ACC AAG ACC TAC CTG GAG TGG CCC ATG GAC GAG Arg Lys Ile Met Asn Thr Lys Thr Tyr Leu Glu Trp Pro Met Asp Glu 735 740 745			2304
30	GCT CAG CGG GAA GGA TTT TGG GTA AAT CTG AGA GCT GCG ATA AAG TCC Ala Gln Arg Glu Gly Phe Trp Val Asn Leu Arg Ala Ala Ile Lys Ser 750 755 760			2352
35	TAG			2355

## (2) INFORMATION FOR SEQ ID NO:4:

40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 784 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
50	Met Pro His Thr Leu Trp Met Val Trp Val Leu Gly Val Ile Ile Ser -22 -20 -15 -10	
	Leu Ser Lys Glu Glu Ser Ser Asn Gln Ala Ser Leu Ser Cys Asp Arg -5 1 5 10	
55	Asn Gly Ile Cys Lys Gly Ser Ser Gly Ser Leu Asn Ser Ile Pro Ser 15 20 25	
	Gly Leu Thr Glu Ala Val Lys Ser Leu Asp Leu Ser Asn Asn Arg Ile 30 35 40	
60	Thr Tyr Ile Ser Asn Ser Asp Leu Gln Arg Cys Val Asn Leu Gln Ala	

		45				50				55					
		Leu Val 60	Leu Thr	Ser	Asn 65	Gly	Ile	Asn Thr	Ile	Glu 70	Glu	Asp	Ser	Phe	
5		Ser Ser 75	Leu Gly	Ser	Leu 80	Glu	His	Leu Asp	Leu 85	Ser Tyr	Asn	Tyr	Leu 90		
10		Ser Asn	Leu Ser	Ser 95	Ser Trp	Phe	Lys	Pro 100	Leu Ser	Ser	Leu Thr	Phe 105			
		Leu Asn	Leu Leu 110	Gly Asn	Pro Tyr	Lys 115	Thr	Leu Gly	Glu Thr	Ser Leu					
15		Phe Ser 125	His Leu	Thr Lys	Leu Gln 130	Ile	Leu Arg	Val Gly 135	Asn Met	Asp					
20		Thr Phe 140	Thr Lys	Ile Gln	Arg Lys 145	Asp	Phe Ala	Gly Leu 150	Thr Phe	Leu					
		Glu Glu 155	Leu Glu	Ile Asp 160	Ala Ser	Asp Leu	Gln Ser	Tyr Glu 170	Pro Lys						
25		Ser Leu	Lys Ser	Ile 175	Gln Asn	Val Ser	His 180	Leu Ile	Leu His	Met 185	Lys				
		Gln His 190	Ile Leu	Leu Leu	Glu Ile	Phe 195	Val Asp	Val Thr	Ser Ser	Val 200					
30		Glu Cys 205	Leu Glu	Leu Arg	Asp Thr	Asp Leu	Asp Thr	Phe His	Phe Ser						
		Glu Leu 220	Ser Thr	Gly Glu	Thr Asn	Ser Leu	Ile Lys	Lys Phe	Thr Phe						
35		Arg Asn 235	Val Lys	Ile Thr	Asp Glu	Ser Leu	Phe 245	Gln Val	Met Lys	Leu 250					
40		Leu Asn	Gln Ile	Ser 255	Gly Leu	Leu Glu	Leu 260	Glu Phe	Asp Asp	Cys Thr 265					
		Leu Asn	Gly Val 270	Gly Asn	Phe Arg	Ala Ser	Asp Asn	Asp Arg	Val Ile						
45		Asp Pro 285	Gly Lys	Val Glu	Thr Leu	Thr 290	Ile Arg	Arg Leu	His Ile	Pro					
		Arg Phe 300	Tyr Leu	Phe Tyr	Asp 305	Leu Ser	Thr Leu	Tyr Ser	Leu Thr	Glu					
50		Arg Val 315	Lys Arg	Ile Thr	Val Glu	Asn Ser	Lys 325	Val Phe	Leu Val	Pro 330					
55		Cys Leu	Leu Ser	Gln 335	His Leu	Lys Ser	Leu 340	Glu Tyr	Leu Asp	Leu Ser					
		Glu Asn	Leu Met 350	Val Glu	Glu Tyr	Leu Lys	Asn Ser	Ala Cys	Glu Asp						
60		Ala Trp 365	Pro Ser	Leu Gln	Thr Leu	Ile 370	Leu Arg	Gln Asn	His Leu	Ala					



Ser Leu Glu Lys Thr Gly Glu Thr Leu Leu Thr Leu Lys Asn Leu Thr  
 380 385 390  
 5 Asn Ile Asp Ile Ser Lys Asn Ser Phe His Ser Met Pro Glu Thr Cys  
 395 400 405 410  
 Gln Trp Pro Glu Lys Met Lys Tyr Leu Asn Leu Ser Ser Thr Arg Ile  
 415 420 425  
 10 His Ser Val Thr Gly Cys Ile Pro Lys Thr Leu Glu Ile Leu Asp Val  
 430 435 440  
 Ser Asn Asn Asn Leu Asn Leu Phe Ser Leu Asn Leu Pro Gln Leu Lys  
 445 450 455  
 Glu Leu Tyr Ile Ser Arg Asn Lys Leu Met Thr Leu Pro Asp Ala Ser  
 460 465 470  
 20 Leu Leu Pro Met Leu Leu Val Leu Lys Ile Ser Arg Asn Ala Ile Thr  
 475 480 485 490  
 Thr Phe Ser Lys Glu Gln Leu Asp Ser Phe His Thr Leu Lys Thr Leu  
 495 500 505  
 25 Glu Ala Gly Gly Asn Asn Phe Ile Cys Ser Cys Glu Phe Leu Ser Phe  
 510 515 520  
 Thr Gln Glu Gln Gln Ala Leu Ala Lys Val Leu Ile Asp Trp Pro Ala  
 525 530 535  
 30 Asn Tyr Leu Cys Asp Ser Pro Ser His Val Arg Gly Gln Gln Val Gln  
 540 545 550  
 35 Asp Val Arg Leu Ser Val Ser Glu Cys His Arg Thr Ala Leu Val Ser  
 555 560 565 570  
 Gly Met Cys Cys Ala Leu Phe Leu Leu Ile Leu Leu Thr Gly Val Leu  
 575 580 585  
 40 Cys His Arg Phe His Gly Leu Trp Tyr Met Lys Met Met Trp Ala Trp  
 590 595 600  
 Leu Gln Ala Lys Arg Lys Pro Arg Lys Ala Pro Ser Arg Asn Ile Cys  
 605 610 615  
 45 Tyr Asp Ala Phe Val Ser Tyr Ser Glu Arg Asp Ala Tyr Trp Val Glu  
 620 625 630  
 50 Asn Leu Met Val Gln Glu Leu Glu Asn Phe Asn Pro Pro Phe Lys Leu  
 635 640 645 650  
 Cys Leu His Lys Arg Asp Phe Ile Pro Gly Lys Trp Ile Ile Asp Asn  
 655 660 665  
 55 Ile Ile Asp Ser Ile Glu Lys Ser His Lys Thr Val Phe Val Leu Ser  
 670 675 680  
 60 Glu Asn Phe Val Lys Ser Glu Trp Cys Lys Tyr Glu Leu Asp Phe Ser  
 685 690 695

His Phe Arg Leu Phe Glu Glu Asn Asn Asp Ala Ala Ile Leu Ile Leu  
 700 705 710  
 5 Leu Glu Pro Ile Glu Lys Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu  
 715 720 725 730  
 Arg Lys Ile Met Asn Thr Lys Thr Tyr Leu Glu Trp Pro Met Asp Glu  
 735 740 745  
 10 Ala Gln Arg Glu Gly Phe Trp Val Asn Leu Arg Ala Ala Ile Lys Ser  
 750 755 760  
 (2) INFORMATION FOR SEQ ID NO:5:  
 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2715 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 20 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 25 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2712  
 (ix) FEATURE:  
 30 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 64..2712  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
 35 ATG AGA CAG ACT TTG CCT TGT ATC TAC TTT TGG GGG GGC CTT TTG CCC 48  
 Met Arg Gln Thr Leu Pro Cys Ile Tyr Phe Trp Gly Gly Leu Leu Pro  
 -21 -20 -15 -10  
 40 TTT GGG ATG CTG TGT GCA TCC TCC ACC ACC AAG TGC ACT GTT AGC CAT 96  
 Phe Gly Met Leu Cys Ala Ser Ser Thr Thr Lys Cys Thr Val Ser His  
 -5 1 5 10  
 45 GAA GTT GCT GAC TGC AGC CAC CTG AAG TTG ACT CAG GTA CCC GAT GAT 144  
 Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp  
 15 20 25  
 CTA CCC ACA AAC ATA ACA GTG TTG AAC CTT ACC CAT AAT CAA CTC AGA 192  
 Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg  
 50 30 35 40  
 AGA TTA CCA GCC GCC AAC TTC ACA AGG TAT AGC CAG CTA ACT AGC TTG 240  
 Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu  
 45 50 55  
 GAT GTA GGA TTT AAC ACC ATC TCA AAA CTG GAG CCA GAA TTG TGC CAG 288  
 Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu Pro Glu Leu Cys Gln  
 60 65 70 75  
 60 AAA CTT CCC ATG TTA AAA GTT TTG AAC CTC CAG CAC AAT GAG CTA TCT 336  
 Lys Leu Pro Met Leu Lys Val Leu Asn Leu Gln His Asn Glu Leu Ser

[illegible]

	TGG CTA AAA TGT TTG GAG CAC CTT AAC ATG GAA GAT AAT GAT ATT CCA	1104
	Trp Leu Lys Cys Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro	
	335 340 345	
5	GGC ATA AAA AGC AAT ATG TTC ACA GGA TTG ATA AAC CTG AAA TAC TTA	1152
	Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu	
	350 355 360	
10	AGT CTA TCC AAC TCC TTT ACA AGT TTG CGA ACT TTG ACA AAT GAA ACA	1200
	Ser Leu Ser Asn Ser Phe Thr Ser Leu Arg Thr Leu Thr Asn Glu Thr	
	365 370 375	
15	TTT GTA TCA CTT GCT CAT TCT CCC TTA CAC ATA CTC AAC CTA ACC AAG	1248
	Phe Val Ser Leu Ala His Ser Pro Leu His Ile Leu Asn Leu Thr Lys	
	380 385 390 395	
20	AAT AAA ATC TCA AAA ATA GAG AGT GAT GCT TTC TCT TGG TTG GGC CAC	1296
	Asn Lys Ile Ser Lys Ile Glu Ser Asp Ala Phe Ser Trp Leu Gly His	
	400 405 410	
25	CTA GAA GTA CTT GAC CTG GGC CTT AAT GAA ATT GGG CAA GAA CTC ACA	1344
	Leu Glu Val Leu Asp Leu Gly Leu Asn Glu Ile Gly Gln Glu Leu Thr	
	415 420 425	
30	GGC CAG GAA TGG AGA GGT CTA GAA AAT ATT TTC GAA ATC TAT CTT TCC	1392
	Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser	
	430 435 440	
35	TAC AAC AAG TAC CTG CAG CTG ACT AGG AAC TCC TTT GCC TTG GTC CCA	1440
	Tyr Asn Lys Tyr Leu Gln Leu Thr Arg Asn Ser Phe Ala Leu Val Pro	
	445 450 455	
40	AGC CTT CAA CGA CTG ATG CTC CGA AGG GTG GCC CTT AAA AAT GTG GAT	1488
	Ser Leu Gln Arg Leu Met Leu Arg Arg Val Ala Leu Lys Asn Val Asp	
	460 465 470 475	
45	AGC TCT CCT TCA CCA TTC CAG CCT CTT CGT AAC TTG ACC ATT CTG GAT	1536
	Ser Ser Pro Ser Pro Phe Gln Pro Leu Arg Asn Leu Thr Ile Leu Asp	
	480 485 490	
50	CTA AGC AAC AAC AAC ATA GCC AAC ATA AAT GAT GAC ATG TTG GAG GGT	1584
	Leu Ser Asn Asn Asn Ile Ala Asn Ile Asn Asp Asp Met Leu Glu Gly	
	495 500 505	
55	CTT GAG AAA CTA GAA ATT CTC GAT TTG CAG CAT AAC AAC TTA GCA CGG	1632
	Leu Glu Lys Leu Glu Ile Leu Asp Leu Gln His Asn Asn Leu Ala Arg	
	510 515 520	
60	CTC TGG AAA CAC GCA AAC CCT GGT GGT CCC ATT TAT TTC CTA AAG GGT	1680
	Leu Trp Lys His Ala Asn Pro Gly Gly Pro Ile Tyr Phe Leu Lys Gly	
	525 530 535	
65	CTG TCT CAC CTC CAC ATC CTT AAC TTG GAG TCC AAC GGC TTT GAC GAG	1728
	Leu Ser His Leu His Ile Leu Asn Leu Glu Ser Asn Gly Phe Asp Glu	
	540 545 550 555	
70	ATC CCA GTT GAG GTC TTC AAG GAT TTA TTT GAA CTA AAG ATC ATC GAT	1776
	Ile Pro Val Glu Val Phe Lys Asp Leu Phe Glu Leu Lys Ile Ile Asp	
	560 565 570	

	TTA GGA TTG AAT AAT TTA AAC ACA CTT CCA GCA TCT GTC TTT AAT AAT	1824
	Leu Gly Leu Asn Asn Leu Asn Thr Leu Pro Ala Ser Val Phe Asn Asn	
	575 580 585	
5	CAG GTG TCT CTA AAG TCA TTG AAC CTT CAG AAG AAT CTC ATA ACA TCC	1872
	Gln Val Ser Leu Lys Ser Leu Asn Leu Gln Lys Asn Leu Ile Thr Ser	
	590 595 600	
10	GTT GAG AAG AAG GTT TTC GGG CCA GCT TTC AGG AAC CTG ACT GAG TTA	1920
	Val Glu Lys Lys Val Phe Gly Pro Ala Phe Arg Asn Leu Thr Glu Leu	
	605 610 615	
15	GAT ATG CGC TTT AAT CCC TTT GAT TGC ACG TGT GAA AGT ATT GCC TGG	1968
	Asp Met Arg Phe Asn Pro Phe Asp Cys Thr Cys Glu Ser Ile Ala Trp	
	620 625 630 635	
20	TTT GTT AAT TGG ATT AAC GAG ACC CAT ACC AAC ATC CCT GAG CTG TCA	2016
	Phe Val Asn Trp Ile Asn Glu Thr His Thr Asn Ile Pro Glu Leu Ser	
	640 645 650	
25	AGC CAC TAC CTT TGC AAC ACT CCA CCT CAC TAT CAT GGG TTC CCA GTG	2064
	Ser His Tyr Leu Cys Asn Thr Pro His Tyr His Gly Phe Pro Val	
	655 660 665	
30	AGA CTT TTT GAT ACA TCA TCT TGC AAA GAC AGT GCC CCC TTT GAA CTC	2112
	Arg Leu Phe Asp Thr Ser Ser Cys Lys Asp Ser Ala Pro Phe Glu Leu	
	670 675 680	
35	TTT TTC ATG ATC AAT ACC AGT ATC CTG TTG ATT TTT ATC TTT ATT GTA	2160
	Phe Phe Met Ile Asn Thr Ser Ile Leu Leu Ile Phe Ile Phe Ile Val	
	685 690 695	
40	CTT CTC ATC CAC TTT GAG GGC TGG AGG ATA TCT TTT TAT TGG AAT GTT	2208
	Leu Leu Ile His Phe Glu Gly Trp Arg Ile Ser Phe Tyr Trp Asn Val	
	700 705 710 715	
45	TCA GTA CAT CGA GTT CTT GGT TTC AAA GAA ATA GAC AGA CAG ACA GAA	2256
	Ser Val His Arg Val Leu Gly Phe Lys Glu Ile Asp Arg Gln Thr Glu	
	720 725 730	
50	CAG TTT GAA TAT GCA GCA TAT ATA ATT CAT GCC TAT AAA GAT AAG GAT	2304
	Gln Phe Glu Tyr Ala Ala Tyr Ile Ile His Ala Tyr Lys Asp Lys Asp	
	735 740 745	
55	TGG GTC TGG GAA CAT TTC TCT TCA ATG GAA AAG GAA GAC CAA TCT CTC	2352
	Trp Val Trp Glu His Phe Ser Ser Met Glu Lys Glu Asp Gln Ser Leu	
	750 755 760	
60	AAA TTT TGT CTG GAA GAA AGG GAC TTT GAG GCG GGT GTT TTT GAA CTA	2400
	Lys Phe Cys Leu Glu Glu Arg Asp Phe Glu Ala Gly Val Phe Glu Leu	
	765 770 775	
65	GAA GCA ATT GTT AAC AGC ATC AAA AGA AGC AGA AAA ATT ATT TTT GTT	2448
	Glu Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe Val	
	780 785 790 795	
70	ATA ACA CAC CAT CTA TTA AAA GAC CCA TTA TGC AAA AGA TTC AAG GTA	2496
	Ile Thr His His Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val	
	800 805 810	
75	CAT CAT GCA GTT CAA CAA GCT ATT GAA CAA AAT CTG GAT TCC ATT ATA	2544

His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile  
 815 820 825

5 TTG GTT TTC CTT GAG GAG ATT CCA GAT TAT AAA CTG AAC CAT GCA CTC 2592  
 Leu Val Phe Leu Glu Glu Ile Pro Asp Tyr Lys Leu Asn His Ala Leu  
 830 835 840

10 TGT TTG CGA AGA GGA ATG TTT AAA TCT CAC TGC ATC TTG AAC TGG CCA 2640  
 Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp Pro  
 845 850 855

15 GTT CAG AAA GAA CGG ATA GGT GCC TTT CGT CAT AAA TTG CAA GTA GCA 2688  
 Val Gln Lys Glu Arg Ile Gly Ala Phe Arg His Lys Leu Gln Val Ala  
 860 865 870 875

CTT GGA TCC AAA AAC TCT GTA CAT TAA 2715  
 Leu Gly Ser Lys Asn Ser Val His  
 880

20 (2) INFORMATION FOR SEQ ID NO:6:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 904 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Arg Gln Thr Leu Pro Cys Ile Tyr Phe Trp Gly Gly Leu Leu Pro  
 -21 -20 -15 -10

35 Phe Gly Met Leu Cys Ala Ser Ser Thr Thr Lys Cys Thr Val Ser His  
 -5 1 5 10

Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp  
 15 20 25

40 Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg  
 30 35 40

45 Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu  
 45 50 55

Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu Pro Glu Leu Cys Gln  
 60 65 70 75

50 Lys Leu Pro Met Leu Lys Val Leu Asn Leu Gln His Asn Glu Leu Ser  
 80 85 90

Gln Leu Ser Asp Lys Thr Phe Ala Phe Cys Thr Asn Leu Thr Glu Leu  
 95 100 105

55 His Leu Met Ser Asn Ser Ile Gln Lys Ile Lys Asn Asn Pro Phe Val  
 110 115 120

60 Lys Gln Lys Asn Leu Ile Thr Leu Asp Leu Ser His Asn Gly Leu Ser  
 125 130 135

Ser Thr Lys Leu Gly Thr Gln Val Gln Leu Glu Asn Leu Gln Glu Leu  
 140 145 150 155  
 5 Leu Leu Ser Asn Asn Lys Ile Gln Ala Leu Lys Ser Glu Glu Leu Asp  
 160 165 170  
 Ile Phe Ala Asn Ser Ser Leu Lys Lys Leu Glu Leu Ser Ser Asn Gln  
 175 180 185  
 10 Ile Lys Glu Phe Ser Pro Gly Cys Phe His Ala Ile Gly Arg Leu Phe  
 190 195 200  
 Gly Leu Phe Leu Asn Asn Val Gln Leu Gly Pro Ser Leu Thr Glu Lys  
 205 210 215  
 15 Leu Cys Leu Glu Leu Ala Asn Thr Ser Ile Arg Asn Leu Ser Leu Ser  
 220 225 230 235  
 Asn Ser Gln Leu Ser Thr Thr Ser Asn Thr Thr Phe Leu Gly Leu Lys  
 240 245 250  
 20 Trp Thr Asn Leu Thr Met Leu Asp Leu Ser Tyr Asn Asn Leu Asn Val  
 255 260 265  
 25 Val Gly Asn Asp Ser Phe Ala Trp Leu Pro Gln Leu Glu Tyr Phe Phe  
 270 275 280  
 Leu Glu Tyr Asn Asn Ile Gln His Leu Phe Ser His Ser Leu His Gly  
 285 290 295  
 30 Leu Phe Asn Val Arg Tyr Leu Asn Leu Lys Arg Ser Phe Thr Lys Gln  
 300 305 310 315  
 Ser Ile Ser Leu Ala Ser Leu Pro Lys Ile Asp Asp Phe Ser Phe Gln  
 320 325 330  
 35 Trp Leu Lys Cys Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro  
 335 340 345  
 40 Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu  
 350 355 360  
 Ser Leu Ser Asn Ser Phe Thr Ser Leu Arg Thr Leu Thr Asn Glu Thr  
 365 370 375  
 45 Phe Val Ser Leu Ala His Ser Pro Leu His Ile Leu Asn Leu Thr Lys  
 380 385 390 395  
 Asn Lys Ile Ser Lys Ile Glu Ser Asp Ala Phe Ser Trp Leu Gly His  
 400 405 410  
 50 Leu Glu Val Leu Asp Leu Gly Leu Asn Glu Ile Gly Gln Glu Leu Thr  
 415 420 425  
 55 Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser  
 430 435 440  
 Tyr Asn Lys Tyr Leu Gln Leu Thr Arg Asn Ser Phe Ala Leu Val Pro  
 445 450 455  
 60 Ser Leu Gln Arg Leu Met Leu Arg Arg Val Ala Leu Lys Asn Val Asp

	460				465				470				475				
5	Ser	Ser	Pro	Ser	Pro	Phe	Gln	Pro	Leu	Arg	Asn	Leu	Thr	Ile	Leu	Asp	
					480					485					490		
	Leu	Ser	Asn	Asn	Asn	Ile	Ala	Asn	Ile	Asn	Asp	Asp	Met	Leu	Glu	Gly	
					495					500					505		
10	Leu	Glu	Lys	Leu	Glu	Ile	Leu	Asp	Leu	Gln	His	Asn	Asn	Leu	Ala	Arg	
					510					515					520		
	Leu	Trp	Lys	His	Ala	Asn	Pro	Gly	Gly	Pro	Ile	Tyr	Phe	Leu	Lys	Gly	
					525					530					535		
15	Leu	Ser	His	Leu	His	Ile	Leu	Asn	Leu	Glu	Ser	Asn	Gly	Phe	Asp	Glu	
					540					545					550		
	Ile	Pro	Val	Glu	Val	Phe	Lys	Asp	Leu	Phe	Glu	Leu	Lys	Ile	Ile	Asp	
					560					565					570		
20	Leu	Gly	Leu	Asn	Asn	Leu	Asn	Thr	Leu	Pro	Ala	Ser	Val	Phe	Asn	Asn	
					575					580					585		
25	Gln	Val	Ser	Leu	Lys	Ser	Leu	Asn	Leu	Gln	Lys	Asn	Leu	Ile	Thr	Ser	
					590					595					600		
	Val	Glu	Lys	Lys	Val	Phe	Gly	Pro	Ala	Phe	Arg	Asn	Leu	Thr	Glu	Leu	
					605					610					615		
30	Asp	Met	Arg	Phe	Asn	Pro	Phe	Asp	Cys	Thr	Cys	Glu	Ser	Ile	Ala	Trp	
					620					625					630		
	Phe	Val	Asn	Trp	Ile	Asn	Glu	Thr	His	Thr	Asn	Ile	Pro	Glu	Leu	Ser	
					640					645					650		
35	Ser	His	Tyr	Leu	Cys	Asn	Thr	Pro	Pro	His	Tyr	His	Gly	Phe	Pro	Val	
					655					660					665		
40	Arg	Leu	Phe	Asp	Thr	Ser	Ser	Cys	Lys	Asp	Ser	Ala	Pro	Phe	Glu	Leu	
					670					675					680		
	Phe	Phe	Met	Ile	Asn	Thr	Ser	Ile	Leu	Leu	Ile	Phe	Ile	Phe	Ile	Val	
					685					690					695		
45	Leu	Leu	Ile	His	Phe	Glu	Gly	Trp	Arg	Ile	Ser	Phe	Tyr	Trp	Asn	Val	
					700					705					710		
	Ser	Val	His	Arg	Val	Leu	Gly	Phe	Lys	Glu	Ile	Asp	Arg	Gln	Thr	Glu	
					720					725					730		
50	Gln	Phe	Glu	Tyr	Ala	Ala	Tyr	Ile	Ile	His	Ala	Tyr	Lys	Asp	Lys	Asp	
					735					740					745		
55	Trp	Val	Trp	Glu	His	Phe	Ser	Ser	Met	Glu	Lys	Glu	Asp	Gln	Ser	Leu	
					750					755					760		
	Lys	Phe	Cys	Leu	Glu	Glu	Arg	Asp	Phe	Glu	Ala	Gly	Val	Phe	Glu	Leu	
					765					770					775		
60	Glu	Ala	Ile	Val	Asn	Ser	Ile	Lys	Arg	Ser	Arg	Lys	Ile	Ile	Phe	Val	
					780					785					790		



Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val  
800 805 810

5 His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile  
815 820 825

Leu Val Phe Leu Glu Glu Ile Pro Asp Tyr Lys Leu Asn His Ala Leu  
830 835 840

10 Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp Pro  
845 850 855

15 Val Gln Lys Glu Arg Ile Gly Ala Phe Arg His Lys Leu Gln Val Ala  
860 865 870 875

Leu Gly Ser Lys Asn Ser Val His  
880

20 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2400 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2397

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAG CTG AAT TTC TAC AAA ATC CCC GAC AAC CTC CCC TTC TCA ACC 48  
Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp Asn Leu Pro Phe Ser Thr  
1 5 10 15

AAG AAC CTG GAC CTG AGC TTT AAT CCC CTG AGG CAT TTA GGC AGC TAT 96  
Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu Gly Ser Tyr  
20 25 30

45 AGC TTC TTC AGT TTC CCA GAA CTG CAG GTG CTG GAT TTA TCC AGG TGT 144  
Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys  
35 40 45

50 GAA ATC CAG ACA ATT GAA GAT GGG GCA TAT CAG AGC CTA AGC CAC CTC 192  
Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu  
50 55 60

55 TCT ACC TTA ATA TTG ACA GGA AAC CCC ATC CAG AGT TTA GCC CTG GGA 240  
Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly  
65 70 75 80

GCC TTT TCT GGA CTA TCA AGT TTA CAG AAG CTG GTG GCT GTG GAG ACA 288  
Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr  
85 90 95

60

	AAT CTA GCA TCT CTA GAG AAC TTC CCC ATT GGA CAT CTC AAA ACT TTG	336
	Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu	
	100 105 110	
5	AAA GAA CTT AAT GTG GCT CAC AAT CTT ATC CAA TCT TTC AAA TTA CCT	384
	Lys Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu Pro	
	115 120 125	
10	GAG TAT TTT TCT AAT CTG ACC AAT CTA GAG CAC TTG GAC CTT TCC AGC	432
	Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser Ser	
	130 135 140	
15	AAC AAG ATT CAA AGT ATT TAT TGC ACA GAC TTG CGG GTT CTA CAT CAA	480
	Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val Leu His Gln	
	145 150 155 160	
20	ATG CCC CTA CTC AAT CTC TCT TTA GAC CTG TCC CTG AAC CCT ATG AAC	528
	Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Met Asn	
	165 170 175	
	TTT ATC CAA CCA GGT GCA TTT AAA GAA ATT AGG CTT CAT AAG CTG ACT	576
	Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr	
	180 185 190	
25	TTA AGA AAT AAT TTT GAT AGT TTA AAT GTA ATG AAA ACT TGT ATT CAA	624
	Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln	
	195 200 205	
30	GGT CTG GCT GGT TTA GAA GTC CAT CGT TTG GTT CTG GGA GAA TTT AGA	672
	Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg	
	210 215 220	
35	AAT GAA GGA AAC TTG GAA AAG TTT GAC AAA TCT GCT CTA GAG GGC CTG	720
	Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu	
	225 230 235 240	
40	TGC AAT TTG ACC ATT GAA GAA TTC CGA TTA GCA TAC TTA GAC TAC TAC	768
	Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr	
	245 250 255	
	CTC GAT GAT ATT ATT GAC TTA TTT AAT TGT TTG ACA AAT GTT TCT TCA	816
	Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser	
	260 265 270	
45	TTT TCC CTG GTG AGT GTG ACT ATT GAA AGG GTA AAA GAC TTT TCT TAT	864
	Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr	
	275 280 285	
50	AAT TTC GGA TGG CAA CAT TTA GAA TTA GTT AAC TGT AAA TTT GGA CAG	912
	Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln	
	290 295 300	
55	TTT CCC ACA TTG AAA CTC AAA TCT CTC AAA AGG CTT ACT TTC ACT TCC	960
	Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser	
	305 310 315 320	
60	AAC AAA GGT GGG AAT GCT TTT TCA GAA GTT GAT CTA CCA AGC CTT GAG	1008
	Asn Lys Gly Gly Asn Ala Phe Ser Glu Val Asp Leu Pro Ser Leu Glu	
	325 330 335	
	TTT CTA GAT CTC AGT AGA AAT GGC TTG AGT TTC AAA GGT TGC TGT TCT	1056

	Phe	Leu	Asp	Leu	Ser	Arg	Asn	Gly	Leu	Ser	Phe	Lys	Gly	Cys	Cys	Ser	
				340					345					350			
5	CAA	AGT	GAT	TTT	GGG	ACA	ACC	AGC	CTA	AAG	TAT	TTA	GAT	CTG	AGC	TTC	1104
	Gln	Ser	Asp	Phe	Gly	Thr	Thr	Ser	Leu	Lys	Tyr	Leu	Asp	Leu	Ser	Phe	
			355					360					365				
10	AAT	GGT	GTT	ATT	ACC	ATG	AGT	TCA	AAC	TTC	TTG	GGC	TTA	GAA	CAA	CTA	1152
	Asn	Gly	Val	Ile	Thr	Met	Ser	Ser	Asn	Phe	Leu	Gly	Leu	Glu	Gln	Leu	
			370				375					380					
15	GAA	CAT	CTG	GAT	TTC	CAG	CAT	TCC	AAT	TTG	AAA	CAA	ATG	AGT	GAG	TTT	1200
	Glu	His	Leu	Asp	Phe	Gln	His	Ser	Asn	Leu	Lys	Gln	Met	Ser	Glu	Phe	
			385			390					395					400	
20	TCA	GTA	TTC	CTA	TCA	CTC	AGA	AAC	CTC	ATT	TAC	CTT	GAC	ATT	TCT	CAT	1248
	Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile	Tyr	Leu	Asp	Ile	Ser	His	
					405					410					415		
25	ACT	CAC	ACC	AGA	GTT	GCT	TTC	AAT	GGC	ATC	TTC	AAT	GGC	TTG	TCC	AGT	1296
	Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile	Phe	Asn	Gly	Leu	Ser	Ser	
				420					425					430			
30	CTC	GAA	GTC	TTG	AAA	ATG	GCT	GGC	AAT	TCT	TTC	CAG	GAA	AAC	TTC	CTT	1344
	Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	Asn	Ser	Phe	Gln	Glu	Asn	Phe	Leu	
			435					440					445				
35	CCA	GAT	ATC	TTC	ACA	GAG	CTG	AGA	AAC	TTG	ACC	TTC	CTG	GAC	CTC	TCT	1392
	Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu	Thr	Phe	Leu	Asp	Leu	Ser	
			450				455					460					
40	CAG	TGT	CAA	CTG	GAG	CAG	TTG	TCT	CCA	ACA	GCA	TTT	AAC	TCA	CTC	TCC	1440
	Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	Ala	Phe	Asn	Ser	Leu	Ser	
			465			470				475					480		
45	AGT	CTT	CAG	GTA	CTA	AAT	ATG	AGC	CAC	AAC	AAC	TTC	TTT	TCA	TTG	GAT	1488
	Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	Asn	Phe	Phe	Ser	Leu	Asp	
				485						490					495		
50	ACG	TTT	CCT	TAT	AAG	TGT	CTG	AAC	TCC	CTC	CAG	GTT	CTT	GAT	TAC	AGT	1536
	Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	Gln	Val	Leu	Asp	Tyr	Ser	
				500					505					510			
55	CTC	AAT	CAC	ATA	ATG	ACT	TCC	AAA	AAA	CAG	GAA	CTA	CAG	CAT	TTT	CCA	1584
	Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	Glu	Leu	Gln	His	Phe	Pro	
			515					520					525				
60	AGT	AGT	CTA	GCT	TTC	TTA	AAT	CTT	ACT	CAG	AAT	GAC	TTT	GCT	TGT	ACT	1632
	Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	Asn	Asp	Phe	Ala	Cys	Thr	
			530				535					540					
65	TGT	GAA	CAC	CAG	AGT	TTC	CTG	CAA	TGG	ATC	AAG	GAC	CAG	AGG	CAG	CTC	1680
	Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	Lys	Asp	Gln	Arg	Gln	Leu	
			545			550					555				560		
70	TTG	GTG	GAA	GTT	GAA	CGA	ATG	GAA	TGT	GCA	ACA	CCT	TCA	GAT	AAG	CAG	1728
	Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala	Thr	Pro	Ser	Asp	Lys	Gln	
					565				570						575		
75	GGC	ATG	CCT	GTG	CTG	AGT	TTG	AAT	ATC	ACC	TGT	CAG	ATG	AAT	AAG	ACC	1776
	Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	Cys	Gln	Met	Asn	Lys	Thr	

	580	585	590	
5	ATC ATT GGT GTG TCG GTC CTC AGT GTG CTT GTA GTA TCT GTT GTA GCA Ile Ile Gly Val Ser Val Leu Ser Val Leu Val Val Ser Val Val Ala 595 600 605			1824
10	GTT CTG GTC TAT AAG TTC TAT TTT CAC CTG ATG CTT CTT GCT GGC TGC Val Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu Ala Gly Cys 610 615 620			1872
15	ATA AAG TAT GGT AGA GGT GAA AAC ATC TAT GAT GCC TTT GTT ATC TAC Ile Lys Tyr Gly Arg Gly Glu Asn Ile Tyr Asp Ala Phe Val Ile Tyr 625 630 635 640			1920
20	TCA AGC CAG GAT GAG GAC TGG GTA AGG AAT GAG CTA GTA AAG AAT TTA Ser Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn Leu 645 650 655			1968
25	GAA GAA GGG GTG CCT CCA TTT CAG CTC TGC CTT CAC TAC AGA GAC TTT Glu Glu Gly Val Pro Pro Phe Gln Leu Cys Leu His Tyr Arg Asp Phe 660 665 670			2016
30	ATT CCC GGT GTG GCC ATT GCT GCC AAC ATC ATC CAT GAA GGT TTC CAT Ile Pro Gly Val Ala Ile Ala Ala Asn Ile Ile His Glu Gly Phe His 675 680 685			2064
35	AAA AGC CGA AAG GTG ATT GTT GTG GTG TCC CAG CAC TTC ATC CAG AGC Lys Ser Arg Lys Val Ile Val Val Val Ser Gln His Phe Ile Gln Ser 690 695 700			2112
40	CGC TGG TGT ATC TTT GAA TAT GAG ATT GCT CAG ACC TGG CAG TTT CTG Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp Gln Phe Leu 705 710 715 720			2160
45	AGC AGT CGT GCT GGT ATC ATC TTC ATT GTC CTG CAG AAG GTG GAG AAG Ser Ser Arg Ala Gly Ile Ile Phe Ile Val Leu Gln Lys Val Glu Lys 725 730 735			2208
50	ACC CTG CTC AGG CAG CAG GTG GAG CTG TAC CGC CTT CTC AGC AGG AAC Thr Leu Leu Arg Gln Gln Val Glu Leu Tyr Arg Leu Leu Ser Arg Asn 740 745 750			2256
55	ACT TAC CTG GAG TGG GAG GAC AGT GTC CTG GGG CGG CAC ATC TTC TGG Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp 755 760 765			2304
60	AGA CGA CTC AGA AAA GCC CTG CTG GAT GGT AAA TCA TGG AAT CCA GAA Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp Asn Pro Glu 770 775 780			2352
65	GGA ACA GTG GGT ACA GGA TGC AAT TGG CAG GAA GCA ACA TCT ATC Gly Thr Val Gly Thr Gly Cys Asn Trp Gln Glu Ala Thr Ser Ile 785 790 795			2397
70	TGA			2400

(2) INFORMATION FOR SEQ ID NO:8:

- 60 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 799 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp Asn Leu Pro Phe Ser Thr  
 1 5 10 15  
 Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu Gly Ser Tyr  
 20 25 30  
 Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys  
 35 40 45  
 Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu  
 50 55 60  
 Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly  
 65 70 75 80  
 Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr  
 85 90 95  
 Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu  
 100 105 110  
 Lys Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu Pro  
 115 120 125  
 Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser Ser  
 130 135 140  
 Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val Leu His Gln  
 145 150 155 160  
 Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Met Asn  
 165 170 175  
 Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr  
 180 185 190  
 Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln  
 195 200 205  
 Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg  
 210 215 220  
 Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu  
 225 230 235 240  
 Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr  
 245 250 255  
 Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser  
 260 265 270  
 Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr  
 275 280 285

Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln  
 290 295 300  
 5 Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser  
 305 310 320  
 Asn Lys Gly Gly Asn Ala Phe Ser Glu Val Asp Leu Pro Ser Leu Glu  
 325 330 335  
 10 Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly Cys Cys Ser  
 340 345 350  
 Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp Leu Ser Phe  
 355 360 365  
 15 Asn Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln Leu  
 370 375 380  
 Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met Ser Glu Phe  
 385 390 395 400  
 20 Ser Val Phe Leu Ser Leu Arg Asn Leu Ile Tyr Leu Asp Ile Ser His  
 405 410 415  
 25 Thr His Thr Arg Val Ala Phe Asn Gly Ile Phe Asn Gly Leu Ser Ser  
 420 425 430  
 Leu Glu Val Leu Lys Met Ala Gly Asn Ser Phe Gln Glu Asn Phe Leu  
 435 440 445  
 30 Pro Asp Ile Phe Thr Glu Leu Arg Asn Leu Thr Phe Leu Asp Leu Ser  
 450 455 460  
 Gln Cys Gln Leu Glu Gln Leu Ser Pro Thr Ala Phe Asn Ser Leu Ser  
 465 470 475 480  
 35 Ser Leu Gln Val Leu Asn Met Ser His Asn Asn Phe Phe Ser Leu Asp  
 485 490 495  
 40 Thr Phe Pro Tyr Lys Cys Leu Asn Ser Leu Gln Val Leu Asp Tyr Ser  
 500 505 510  
 Leu Asn His Ile Met Thr Ser Lys Lys Gln Glu Leu Gln His Phe Pro  
 515 520 525  
 45 Ser Ser Leu Ala Phe Leu Asn Leu Thr Gln Asn Asp Phe Ala Cys Thr  
 530 535 540  
 Cys Glu His Gln Ser Phe Leu Gln Trp Ile Lys Asp Gln Arg Gln Leu  
 545 550 555 560  
 50 Leu Val Glu Val Glu Arg Met Glu Cys Ala Thr Pro Ser Asp Lys Gln  
 565 570 575  
 55 Gly Met Pro Val Leu Ser Leu Asn Ile Thr Cys Gln Met Asn Lys Thr  
 580 585 590  
 Ile Ile Gly Val Ser Val Leu Ser Val Leu Val Val Ser Val Val Ala  
 595 600 605  
 60 Val Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu Ala Gly Cys

610                                  615                                  620

Ile Lys Tyr Gly Arg Gly Glu Asn Ile Tyr Asp Ala Phe Val Ile Tyr  
625                                  630                                  635                                  640

5 Ser Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn Leu  
645                                  650                                  655

10 Glu Glu Gly Val Pro Pro Phe Gln Leu Cys Leu His Tyr Arg Asp Phe  
660                                  665                                  670

Ile Pro Gly Val Ala Ile Ala Ala Asn Ile Ile His Glu Gly Phe His  
675                                  680                                  685

15 Lys Ser Arg Lys Val Ile Val Val Val Ser Gln His Phe Ile Gln Ser  
690                                  695                                  700

Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp Gln Phe Leu  
705                                  710                                  715                                  720

20 Ser Ser Arg Ala Gly Ile Ile Phe Ile Val Leu Gln Lys Val Glu Lys  
725                                  730                                  735

Thr Leu Leu Arg Gln Gln Val Glu Leu Tyr Arg Leu Leu Ser Arg Asn  
740                                  745                                  750

25 Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp  
755                                  760                                  765

30 Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp Asn Pro Glu  
770                                  775                                  780

Gly Thr Val Gly Thr Gly Cys Asn Trp Gln Glu Ala Thr Ser Ile  
785                                  790                                  795

35

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..1095

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

55 TGT TGG GAT GGT TTT GAG GGA CTT TCT CAT CTT CAA GTT CTG TAT TTG 48  
Cys Trp Asp Val Phe Glu Gly Leu Ser His Leu Gln Val Leu Tyr Leu  
1 5 10 15

AAT CAT AAC TAT CTT AAT TCC CTT CCA CCA GGA GTA TTT AGC CAT CTG 96  
Asn His Asn Tyr Leu Asn Ser Leu Pro Gly Val Phe Ser His Leu  
20 25 30

60

	ACT GCA TTA AGG GGA CTA AGC CTC AAC TCC AAC AGG CTG ACA GTT CTT	144
	Thr Ala Leu Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu	
	35 40 45	
5	TCT CAC AAT GAT TTA CCT GCT AAT TTA GAG ATC CTG GAC ATA TCC AGG	192
	Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg	
	50 55 60	
10	AAC CAG CTC CTA GCT CCT AAT CCT GAT GTA TTT GTA TCA CTT AGT GTC	240
	Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val	
	65 70 75 80	
15	TTG GAT ATA ACT CAT AAC AAG TTC ATT TGT GAA TGT GAA CTT AGC ACT	288
	Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr	
	85 90 95	
20	TTT ATC AAT TGG CTT AAT CAC ACC AAT GTC ACT ATA GCT GGG CCT CCT	336
	Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro	
	100 105 110	
	GCA GAC ATA TAT TGT GTG TAC CCT GAC TCG TTC TCT GGG GTT TCC CTC	384
	Ala Asp Ile Tyr Cys Val Tyr Pro Asp Ser Phe Ser Gly Val Ser Leu	
	115 120 125	
25	TTC TCT CTT TCC ACG GAA GGT TGT GAT GAA GAG GAA GTC TTA AAG TCC	432
	Phe Ser Leu Ser Thr Glu Gly Cys Asp Glu Glu Glu Val Leu Lys Ser	
	130 135 140	
30	CTA AAG TTC TCC CTT TTC ATT GTA TGC ACT GTC ACT CTG ACT CTG TTC	480
	Leu Lys Phe Ser Leu Phe Ile Val Cys Thr Val Thr Leu Thr Leu Phe	
	145 150 155 160	
35	CTC ATG ACC ATC CTC ACA GTC ACA AAG TTC CGG GGC TTC TGT TTT ATC	528
	Leu Met Thr Ile Leu Thr Val Thr Lys Phe Arg Gly Phe Cys Phe Ile	
	165 170 175	
40	TGT TAT AAG ACA GCC CAG AGA CTG GTG TTC AAG GAC CAT CCC CAG GGC	576
	Cys Tyr Lys Thr Ala Gln Arg Leu Val Phe Lys Asp His Pro Gln Gly	
	180 185 190	
	ACA GAA CCT GAT ATG TAC AAA TAT GAT GCC TAT TTG TGC TTC AGC AGC	624
	Thr Glu Pro Asp Met Tyr Lys Tyr Asp Ala Tyr Leu Cys Phe Ser Ser	
	195 200 205	
45	AAA GAC TTC ACA TGG GTG CAG AAT GCT TTG CTC AAA CAC CTG GAC ACT	672
	Lys Asp Phe Thr Trp Val Gln Asn Ala Leu Leu Lys His Leu Asp Thr	
	210 215 220	
50	CAA TAC AGT GAC CAA AAC AGA TTC AAC CTG TGC TTT GAA GAA AGA GAC	720
	Gln Tyr Ser Asp Gln Asn Arg Phe Asn Leu Cys Phe Glu Glu Arg Asp	
	225 230 235 240	
55	TTT GTC CCA GGA GAA AAC CGC ATT GCC AAT ATC CAG GAT GCC ATC TGG	768
	Phe Val Pro Gly Glu Asn Arg Ile Ala Asn Ile Gln Asp Ala Ile Trp	
	245 250 255	
60	AAC AGT AGA AAG ATC GTT TGT CTT GTG AGC AGA CAC TTC CTT AGA GAT	816
	Asn Ser Arg Lys Ile Val Cys Leu Val Ser Arg His Phe Leu Arg Asp	
	260 265 270	
	GGC TGG TGC CTT GAA GCC TTC AGT TAT GCC CAG GGC AGG TGC TTA TCT	864



	Gly Trp Cys Leu Glu Ala Phe Ser Tyr Ala Gln Gly Arg Cys Leu Ser	
	275 280 285	
5	GAC CTT AAC AGT GCT CTC ATC ATG GTG GTG GTT GGG TCC TTG TCC CAG Asp Leu Asn Ser Ala Leu Ile Met Val Val Val Gly Ser Leu Ser Gln	912
	290 295 300	
10	TAC CAG TTG ATG AAA CAT CAA TCC ATC AGA GGC TTT GTA CAG AAA CAG Tyr Gln Leu Met Lys His Gln Ser Ile Arg Gly Phe Val Gln Lys Gln	960
	305 310 315	
15	CAG TAT TTG AGG TGG CCT GAG GAT CTC CAG GAT GTT GGC TGG TTT CTT Gln Tyr Leu Arg Trp Pro Glu Asp Leu Gln Asp Val Gly Trp Phe Leu	1008
	325 330 335	
20	CAT AAA CTC TCT CAA CAG ATA CTA AAG AAA GAA AAG GAA AAG AAG AAA His Lys Leu Ser Gln Gln Ile Leu Lys Lys Glu Lys Glu Lys Lys Lys	1056
	340 345 350	
25	GAC AAT AAC ATT CCG TTG CAA ACT GTA GCA ACC ATC TCC TAATCAAAGG Asp Asn Asn Ile Pro Leu Gln Thr Val Ala Thr Ile Ser	1105
	355 360 365	
30	AGCAATTTC AACCTATCTC AAGCCACAAA TAACCTCTCA CTTTGTATTT GCACCAAGTT ATCATTTTGG GGTCTCTCTT GGAGGTTTTT TTTTCTTTT TGCTACTATG AAAACAACAT AAATCTCTCA ATTTTCGTAT CAAAAA AAAA AAAA TGGCGGCCGC	1165 1225 1275
	(2) INFORMATION FOR SEQ ID NO:10:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 365 amino acids	
	(B) TYPE: amino acid	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
	Cys Trp Asp Val Phe Glu Gly Leu Ser His Leu Gln Val Leu Tyr Leu	
	1 5 10 15	
45	Asn His Asn Tyr Leu Asn Ser Leu Pro Pro Gly Val Phe Ser His Leu	
	20 25 30	
50	Thr Ala Leu Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu	
	35 40 45	
55	Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg	
	50 55 60	
60	Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val	
	65 70 75 80	
	Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr	
	85 90 95	
60	Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro	
	100 105 110	

Ala Asp Ile Tyr Cys Val Tyr Pro Asp Ser Phe Ser Gly Val Ser Leu  
115 120 125

5 Phe Ser Leu Ser Thr Glu Gly Cys Asp Glu Glu Glu Val Leu Lys Ser  
130 135 140

Leu Lys Phe Ser Leu Phe Ile Val Cys Thr Val Thr Leu Thr Leu Phe  
145 150 155 160

10 Leu Met Thr Ile Leu Thr Val Thr Lys Phe Arg Gly Phe Cys Phe Ile  
165 170 175

Cys Tyr Lys Thr Ala Gln Arg Leu Val Phe Lys Asp His Pro Gln Gly  
180 185 190

15 Thr Glu Pro Asp Met Tyr Lys Tyr Asp Ala Tyr Leu Cys Phe Ser Ser  
195 200 205

20 Lys Asp Phe Thr Trp Val Gln Asn Ala Leu Leu Lys His Leu Asp Thr  
210 215 220

Gln Tyr Ser Asp Gln Asn Arg Phe Asn Leu Cys Phe Glu Glu Arg Asp  
225 230 235 240

25 Phe Val Pro Gly Glu Asn Arg Ile Ala Asn Ile Gln Asp Ala Ile Trp  
245 250 255

Asn Ser Arg Lys Ile Val Cys Leu Val Ser Arg His Phe Leu Arg Asp  
260 265 270

30 Gly Trp Cys Leu Glu Ala Phe Ser Tyr Ala Gln Gly Arg Cys Leu Ser  
275 280 285

35 Asp Leu Asn Ser Ala Leu Ile Met Val Val Val Gly Ser Leu Ser Gln  
290 295 300

Tyr Gln Leu Met Lys His Gln Ser Ile Arg Gly Phe Val Gln Lys Gln  
305 310 315 320

40 Gln Tyr Leu Arg Trp Pro Glu Asp Leu Gln Asp Val Gly Trp Phe Leu  
325 330 335

His Lys Leu Ser Gln Gln Ile Leu Lys Lys Glu Lys Glu Lys Lys Lys  
340 345 350

45 Asp Asn Asn Ile Pro Leu Gln Thr Val Ala Thr Ile Ser  
355 360 365

50 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3138 base pairs  
55 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

60

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..3135

(ix) FEATURE:  
5 (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 67..3135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10	ATG TGG ACA CTG AAG AGA CTA ATT CTT ATC CTT TTT AAC ATA ATC CTA	48
	Met Trp Thr Leu Lys Arg Leu Ile Leu Ile Leu Phe Asn Ile Ile Leu	
	-22 -20 -15 -10	
15	ATT TCC AAA CTC CTT GGG GCT AGA TGG TTT CCT AAA ACT CTG CCC TGT	96
	Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys Thr Leu Pro Cys	
	-5 1 5 10	
20	GAT GTC ACT CTG GAT GTT CCA AAG AAC CAT GTG ATC GTG GAC TGC ACA	144
	Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile Val Asp Cys Thr	
	15 20 25	
25	GAC AAG CAT TTG ACA GAA ATT CCT GGA GGT ATT CCC ACG AAC ACC ACG	192
	Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro Thr Asn Thr Thr	
	30 35 40	
30	AAC CTC ACC CTC ACC ATT AAC CAC ATA CCA GAC ATC TCC CCA GCG TCC	240
	Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile Ser Pro Ala Ser	
	45 50 55	
35	TTT CAC AGA CTG GAC CAT CTG GTA GAG ATC GAT TTC AGA TGC AAC TGT	288
	Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe Arg Cys Asn Cys	
	60 65 70	
40	GTA CCT ATT CCA CTG GGG TCA AAA AAC AAC ATG TGC ATC AAG AGG CTG	336
	Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu	
	75 80 85 90	
45	CAG ATT AAA CCC AGA AGC TTT AGT GGA CTC ACT TAT TTA AAA TCC CTT	384
	Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu	
	95 100 105	
50	TAC CTG GAT GGA AAC CAG CTA CTA GAG ATA CCG CAG GGC CTC CCG CCT	432
	Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro	
	110 115 120	
55	AGC TTA CAG CTT CTC AGC CTT GAG GCC AAC AAC ATC TTT TCC ATC AGA	480
	Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg	
	125 130 135	
60	AAA GAG AAT CTA ACA GAA CTG GCC AAC ATA GAA ATA CTC TAC CTG GGC	528
	Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly	
	140 145 150	
65	CAA AAC TGT TAT TAT CGA AAT CCT TGT TAT GTT TCA TAT TCA ATA GAG	576
	Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile Glu	
	155 160 165 170	
70	AAA GAT GCC TTC CTA AAC TTG ACA AAG TTA AAA GTG CTC TCC CTG AAA	624
	Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser Leu Lys	
	175 180 185	

5	GAT AAC AAT GTC ACA GCC GTC CCT ACT GTT TTG CCA TCT ACT TTA ACA Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser Thr Leu Thr	672
	190 195 200	
10	GAA CTA TAT CTC TAC AAC AAC ATG ATT GCA AAA ATC CAA GAA GAT GAT Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile Gln Glu Asp Asp	720
	205 210 215	
15	TTT AAT AAC CTC AAC CAA TTA CAA ATT CTT GAC CTA AGT GGA AAT TGC Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu Ser Gly Asn Cys	768
	220 225 230	
20	CCT CGT TGT TAT AAT GCC CCA TTT CCT TGT GCG CCG TGT AAA AAT AAT Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys Ala Pro Cys Lys Asn Asn	816
	235 240 245 250	
25	TCT CCC CTA CAG ATC CCT GTA AAT GCT TTT GAT GCG CTG ACA GAA TTA Ser Pro Leu Gln Ile Pro Val Asn Ala Phe Asp Ala Leu Thr Glu Leu	864
	255 260 265	
30	AAA GTT TTA CGT CTA CAC AGT AAC TCT CTT CAG CAT GTG CCC CCA AGA Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His Val Pro Pro Arg	912
	270 275 280	
35	TGG TTT AAG AAC ATC AAC AAA CTC CAG GAA CTG GAT CTG TCC CAA AAC Trp Phe Lys Asn Ile Asn Lys Leu Gln Glu Leu Asp Leu Ser Gln Asn	960
	285 290 295	
40	TTC TTG GCC AAA GAA ATT GGG GAT GCT AAA TTT CTG CAT TTT CTC CCC Phe Leu Ala Lys Glu Ile Gly Asp Ala Lys Phe Leu His Phe Leu Pro	1008
	300 305 310	
45	AGC CTC ATC CAA TTG GAT CTG TCT TTC AAT TTT GAA CTT CAG GTC TAT Ser Leu Ile Gln Leu Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr	1056
	315 320 325 330	
50	CGT GCA TCT ATG AAT CTA TCA CAA GCA TTT TCT TCA CTG AAA AGC CTG Arg Ala Ser Met Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu	1104
	335 340 345	
55	AAA ATT CTG CGG ATC AGA GGA TAT GTC TTT AAA GAG TTG AAA AGC TTT Lys Ile Leu Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe	1152
	350 355 360	
60	AAC CTC TCG CCA TTA CAT AAT CTT CAA AAT CTT GAA GTT CTT GAT CTT Asn Leu Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu	1200
	365 370 375	
65	GGC ACT AAC TTT ATA AAA ATT GCT AAC CTC AGC ATG TTT AAA CAA TTT Gly Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	1248
	380 385 390	
70	AAA AGA CTG AAA GTC ATA GAT CTT TCA GTG AAT AAA ATA TCA CCT TCA Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro Ser	1296
	395 400 405 410	
75	GGA GAT TCA AGT GAA GTT GGC TTC TGC TCA AAT GCC AGA ACT TCT GTA Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr Ser Val	1344
	415 420 425	

	GAA AGT TAT GAA CCC CAG GTC CTG GAA CAA TTA CAT TAT TTC AGA TAT	1392
	Glu Ser Tyr 430 Glu Pro Gln Val Leu 435 Glu Gln Leu His Tyr 440 Phe Arg Tyr	
5	GAT AAG TAT GCA AGG AGT TGC AGA TTC AAA AAC AAA GAG GCT TCT TTC	1440
	Asp Lys Tyr 445 Ala Arg Ser Cys Arg Phe Lys Asn Lys Glu Ala Ser Phe	
10	ATG TCT GTT AAT GAA AGC TGC TAC AAG TAT GGG CAG ACC TTG GAT CTA	1488
	Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly Gln Thr Leu Asp Leu	
	460 465 470	
15	AGT AAA AAT AGT ATA TTT TTT GTC AAG TCC TCT GAT TTT CAG CAT CTT	1536
	Ser Lys Asn Ser Ile Phe Phe Val Lys Ser Ser Asp Phe Gln His Leu	
	475 480 485 490	
20	TCT TTC CTC AAA TGC CTG AAT CTG TCA GGA AAT CTC ATT AGC CAA ACT	1584
	Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn Leu Ile Ser Gln Thr	
	495 500 505	
	CTT AAT GGC AGT GAA TTC CAA CCT TTA GCA GAG CTG AGA TAT TTG GAC	1632
	Leu Asn Gly Ser Glu Phe Gln Pro Leu Ala Glu Leu Arg Tyr Leu Asp	
	510 515 520	
25	TTC TCC AAC AAC CGG CTT GAT TTA CTC CAT TCA ACA GCA TTT GAA GAG	1680
	Phe Ser 525 Asn Arg Leu Asp Leu Leu His Ser Thr Ala Phe Glu Glu	
	530 535	
30	CTT CAC AAA CTG GAA GTT CTG GAT ATA AGC AGT AAT AGC CAT TAT TTT	1728
	Leu His 540 Lys Leu Glu Val Leu Asp Ile Ser Ser Asn Ser His Tyr Phe	
	545 550	
35	CAA TCA GAA GGA ATT ACT CAT ATG CTA AAC TTT ACC AAG AAC CTA AAG	1776
	Gln Ser Glu Gly Ile Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys	
	555 560 565 570	
40	GTT CTG CAG AAA CTG ATG ATG AAC GAC AAT GAC ATC TCT TCC TCC ACC	1824
	Val Leu Gln Lys Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr	
	575 580 585	
	AGC AGG ACC ATG GAG AGT GAG TCT CTT AGA ACT CTG GAA TTC AGA GGA	1872
	Ser Arg Thr 590 Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly	
	600	
45	AAT CAC TTA GAT GTT TTA TGG AGA GAA GGT GAT AAC AGA TAC TTA CAA	1920
	Asn His 605 Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln	
	610 615	
50	TTA TTC AAG AAT CTG CTA AAA TTA GAG GAA TTA GAC ATC TCT AAA AAT	1968
	Leu Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn	
	620 625 630	
55	TCC CTA AGT TTC TTG CCT TCT GGA GTT TTT GAT GGT ATG CCT CCA AAT	2016
	Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro Asn	
	635 640 645 650	
	CTA AAG AAT CTC TCT TTG GCC AAA AAT GGG CTC AAA TCT TTC AGT TGG	2064
	Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe Ser Trp	
	655 660 665	
60	AAG AAA CTC CAG TGT CTA AAG AAC CTG GAA ACT TTG GAC CTC AGC CAC	2112

	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu	Asp	Leu	Ser	His	
				670					675					680			
5	AAC	CAA	CTG	ACC	ACT	GTC	CCT	GAG	AGA	TTA	TCC	AAC	TGT	TCC	AGA	AGC	2160
	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn	Cys	Ser	Arg	Ser	
			685					690					695				
10	CTC	AAG	AAT	CTG	ATT	CTT	AAG	AAT	AAT	CAA	ATC	AGG	AGT	CTG	ACG	AAG	2208
	Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	Arg	Ser	Leu	Thr	Lys	
			700				705					710					
15	TAT	TTT	CTA	CAA	GAT	GCC	TTC	CAG	TTG	CGA	TAT	CTG	GAT	CTC	AGC	TCA	2256
	Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	Ser	
			715			720					725					730	
20	AAT	AAA	ATC	CAG	ATG	ATC	CAA	AAG	ACC	AGC	TTC	CCA	GAA	AAT	GTC	CTC	2304
	Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr	Ser	Phe	Pro	Glu	Asn	Val	Leu	
					735					740					745		
25	AAC	AAT	CTG	AAG	ATG	TTG	CTT	TTG	CAT	CAT	AAT	CGG	TTT	CTG	TGC	ACC	2352
	Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu	His	His	Asn	Arg	Phe	Leu	Cys	Thr	
					750				755								
30	TGT	GAT	GCT	GTG	TGG	TTT	GTC	TGG	TGG	GTT	AAC	CAT	ACG	GAG	GTG	ACT	2400
	Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn	His	Thr	Glu	Val	Thr	
					765			770					775				
35	ATT	CCT	TAC	CTG	GCC	ACA	GAT	GTG	ACT	TGT	GTG	GGG	CCA	GGA	GCA	CAC	2448
	Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	Gly	Pro	Gly	Ala	His	
					780			785				790					
40	AAG	GGC	CAA	AGT	GTG	ATC	TCC	CTG	GAT	CTG	TAC	ACC	TGT	GAG	TTA	GAT	2496
	Lys	Gly	Gln	Ser	Val	Ile	Ser	Leu	Asp	Leu	Tyr	Thr	Cys	Glu	Leu	Asp	
						800					805				810		
45	CTG	ACT	AAC	CTG	ATT	CTG	TTC	TCA	CTT	TCC	ATA	TCT	GTA	TCT	CTC	TTT	2544
	Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	
					815					820					825		
50	CTC	ATG	GTG	ATG	ATG	ACA	GCA	AGT	CAC	CTC	TAT	TTC	TGG	GAT	GTG	TGG	2592
	Leu	Met	Val	Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp	
					830				835					840			
55	TAT	ATT	TAC	CAT	TTC	TGT	AAG	GCC	AAG	ATA	AAG	GGG	TAT	CAG	OGT	CTA	2640
	Tyr	Ile	Thr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu	
					845			850					855				
60	ATA	TCA	CCA	GAC	TGT	TGC	TAT	GAT	GCT	TTT	ATT	GTG	TAT	GAC	ACT	AAA	2688
	Ile	Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys	
							865					870					
65	GAC	CCA	GCT	GTG	ACC	GAG	TGG	GTT	TTG	GCT	GAG	CTG	GTG	GCC	AAA	CTG	2736
	Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys	Leu	
						880					885				890		
70	GAA	GAC	CCA	AGA	GAG	AAA	CAT	TTT	AAT	TTA	TGT	CTC	GAG	GAA	AGG	GAC	2784
	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu	Glu	Glu	Arg	Asp	
						895				900					905		
75	TGG	TTA	CCA	GGG	CAG	CCA	GTT	CTG	GAA	AAC	CTT	TCC	CAG	AGC	ATA	CAG	2832
	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln	Ser	Ile	Gln	

	910	915	920	
5	CTT AGC AAA AAG ACA GTG TTT GTG ATG ACA GAC AAG TAT GCA AAG ACT Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys Tyr Ala Lys Thr	2880		
	925	930	935	
10	GAA AAT TTT AAG ATA GCA TTT TAC TTG TCC CAT CAG AGG CTC ATG GAT Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln Arg Leu Met Asp	2928		
	940	945	950	
	GAA AAA GTT GAT GTG ATT ATC TTG ATA TTT CTT GAG AAG CCC TTT CAG Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu Lys Pro Phe Gln	2976		
	955	960	965	970
15	AAG TCC AAG TTC CTC CAG CTC CGG AAA AGG CTC TGT GGG AGT TCT GTC Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys Gly Ser Ser Val	3024		
	975	980	985	
20	CTT GAG TGG CCA ACA AAC CCG CAA GCT CAC CCA TAC TTC TGG CAG TGT Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro Tyr Phe Trp Gln Cys	3072		
	990	995	1000	
25	CTA AAG AAC GCC CTG GCC ACA GAC AAT CAT GTG GCC TAT AGT CAG GTG Leu Lys Asn Ala Leu Ala Thr Asp Asn His Val Ala Tyr Ser Gln Val	3120		
	1005	1010	1015	
	TTC AAG GAA ACG GTC TAG Phe Lys Glu Thr Val	3138		
	1020			
30				
	(2) INFORMATION FOR SEQ ID NO:12:			
	(i) SEQUENCE CHARACTERISTICS:			
35	(A) LENGTH: 1045 amino acids			
	(B) TYPE: amino acid			
	(D) TOPOLOGY: linear			
	(ii) MOLECULE TYPE: protein			
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:			
	Met Trp Thr Leu Lys Arg Leu Ile Leu Ile Leu Phe Asn Ile Ile Leu			
	-22 -20 -15 -10			
45	Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys Thr Leu Pro Cys			
	-5 1 5 10			
50	Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile Val Asp Cys Thr			
	15 20 25			
	Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro Thr Asn Thr Thr			
	30 35 40			
55	Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile Ser Pro Ala Ser			
	45 50 55			
	Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe Arg Cys Asn Cys			
	60 65 70			
60	Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu			

	75		80		85		90
	Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu						
			95		100		105
5	Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro			110	115	120	
	Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg			125	130	135	
10	Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly			140	145	150	
	Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile Glu			155	160	165	170
	Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser Leu Lys			175	180	185	
20	Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser Thr Leu Thr			190	195	200	
	Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile Gln Glu Asp Asp			205	210	215	
25	Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu Ser Gly Asn Cys			220	225	230	
	Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys Ala Pro Cys Lys Asn Asn			235	240	245	250
	Ser Pro Leu Gln Ile Pro Val Asn Ala Phe Asp Ala Leu Thr Glu Leu			255	260	265	
35	Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His Val Pro Pro Arg			270	275	280	
	Trp Phe Lys Asn Ile Asn Lys Leu Gln Glu Leu Asp Leu Ser Gln Asn			285	290	295	
40	Phe Leu Ala Lys Glu Ile Gly Asp Ala Lys Phe Leu His Phe Leu Pro			300	305	310	
	Ser Leu Ile Gln Leu Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr			315	320	325	330
	Arg Ala Ser Met Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu			335	340	345	
50	Lys Ile Leu Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe			350	355	360	
	Asn Leu Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu			365	370	375	
55	Gly Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe			380	385	390	
	Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro Ser			395	400	405	410



Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr Ser Val  
 415 420 425  
 5 Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr Phe Arg Tyr  
 430 435 440  
 Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys Glu Ala Ser Phe  
 445 450 455  
 10 Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly Gln Thr Leu Asp Leu  
 460 465 470  
 15 Ser Lys Asn Ser Ile Phe Phe Val Lys Ser Ser Asp Phe Gln His Leu  
 475 480 485 490  
 Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn Leu Ile Ser Gln Thr  
 495 500 505  
 20 Leu Asn Gly Ser Glu Phe Gln Pro Leu Ala Glu Leu Arg Tyr Leu Asp  
 510 515 520  
 Phe Ser Asn Asn Arg Leu Asp Leu Leu His Ser Thr Ala Phe Glu Glu  
 525 530 535  
 25 Leu His Lys Leu Glu Val Leu Asp Ile Ser Ser Asn Ser His Tyr Phe  
 540 545 550  
 30 Gln Ser Glu Gly Ile Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys  
 555 560 565 570  
 Val Leu Gln Lys Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr  
 575 580 585  
 35 Ser Arg Thr Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly  
 590 595 600  
 Asn His Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln  
 605 610 615  
 40 Leu Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn  
 620 625 630  
 45 Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro Asn  
 635 640 645 650  
 Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe Ser Trp  
 655 660 665  
 50 Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp Leu Ser His  
 670 675 680  
 Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn Cys Ser Arg Ser  
 685 690 695  
 55 Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile Arg Ser Leu Thr Lys  
 700 705 710  
 60 Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg Tyr Leu Asp Leu Ser Ser  
 715 720 725 730

Asn Lys Ile Gln Met Ile Gln Lys Thr Ser Phe Pro Glu Asn Val Leu  
 735 740 745  
 5 Asn Asn Leu Lys Met Leu Leu Leu His His Asn Arg Phe Leu Cys Thr  
 750 755 760  
 Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His Thr Glu Val Thr  
 765 770 775  
 10 Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly Pro Gly Ala His  
 780 785 790  
 Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp  
 795 800 805  
 15 Leu Thr Asn Leu Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe  
 815 820 825  
 20 Leu Met Val Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp  
 830 835 840  
 Tyr Ile Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu  
 845 850 855  
 25 Ile Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys  
 860 865 870  
 Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys Leu  
 875 880 885  
 30 Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu Arg Asp  
 895 900 905  
 35 Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln Ser Ile Gln  
 910 915 920  
 Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys Tyr Ala Lys Thr  
 925 930 935  
 40 Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln Arg Leu Met Asp  
 940 945 950  
 Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu Lys Pro Phe Gln  
 955 960 965  
 45 Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys Gly Ser Ser Val  
 975 980 985  
 50 Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro Tyr Phe Trp Gln Cys  
 990 995 1000  
 Leu Lys Asn Ala Leu Ala Thr Asp Asn His Val Ala Tyr Ser Gln Val  
 1005 1010 1015  
 55 Phe Lys Glu Thr Val  
 1020

(2) INFORMATION FOR SEQ ID NO:13:

- 60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 180 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

10 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

15	CTT GGA AAA CCT CTT CAG AAG TCT AAG TTT CTT CAG CTC AGG AAG AGA	48
	Leu Gly Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg	
	1 5 10 15	
20	CTC TGC AGG AGC TCT GTC CTT GAG TGG CCT GCA AAT CCA CAG GCT CAC	96
	Leu Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His	
	20 25 30	
	CCA TAC TTC TGG CAG TGC CTG AAA AAT GCC CTG ACC ACA GAC AAT CAT	144
25	Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn His	
	35 40 45	
	GTG GCT TAT AGT CAA ATG TTC AAG GAA ACA GTC TAG	180
	Val Ala Tyr Ser Gln Met Phe Lys Glu Thr Val	
	50 55	

30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 59 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

45	Leu Gly Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg
	1 5 10 15
	Leu Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His
	20 25 30
50	Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn His
	35 40 45
	Val Ala Tyr Ser Gln Met Phe Lys Glu Thr Val
	50 55

55 (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 990 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 2..988

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

G AAT TCC AGA CTT ATA AAC TTG AAA AAT CTC TAT TTG GCC TGG AAC	46
Asn Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn	
1 5 10 15	
15 TGC TAT TTT AAC AAA GTT TGC GAG AAA ACT AAC ATA GAA GAT GGA GTA	94
Cys Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val	
20 20 25 30	
20 TTT GAA ACG CTG ACA AAT TTG GAG TTG CTA TCA CTA TCT TTC AAT TCT	142
Phe Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser	
35 40 45	
25 CTT TCA CAT GTG CCA CCC AAA CTG CCA AGC TCC CTA CGC AAA CTT TTT	190
Leu Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe	
50 55 60	
30 CTG AGC AAC ACC CAG ATC AAA TAC ATT AGT GAA GAA GAT TTC AAG GGA	238
Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly	
65 70 75	
35 TTG ATA AAT TTA ACA TTA CTA GAT TTA AGC GGG AAC TGT CCG AGG TGC	286
Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys	
80 85 90 95	
40 TTC AAT GCC CCA TTT CCA TGC GTG CCT TGT GAT GGT GGT GCT TCA ATT	334
Phe Asn Ala Pro Phe Pro Cys Val Pro Cys Asp Gly Gly Ala Ser Ile	
100 105 110	
45 AAT ATA GAT CGT TTT GCT TTT CAA AAC TTG ACC CAA CTT CGA TAC CTA	382
Asn Ile Asp Arg Phe Ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr Leu	
115 120 125	
50 AAC CTC TCT AGC ACT TCC CTC AGG AAG ATT AAT GCT GCC TGG TTT AAA	430
Asn Leu Ser Ser Thr Ser Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys	
130 135 140	
55 AAT ATG CCT CAT CTG AAG GTG CTG GAT CTT GAA TTC AAC TAT TTA GTG	478
Asn Met Pro His Leu Lys Val Leu Asp Leu Glu Phe Asn Tyr Leu Val	
145 150 155	
60 GGA GAA ATA GCC TCT GGG GCA TTT TTA ACG ATG CTG CCC CGC TTA GAA	526
Gly Glu Ile Ala Ser Gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu	
160 165 170 175	
65 ATA CTT GAC TTG TCT TTT AAC TAT ATA AAG GGG AGT TAT CCA CAG CAT	574
Ile Leu Asp Leu Ser Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His	
180 185 190	
70 ATT AAT ATT TCC AGA AAC TTC TCT AAA CTT TTG TCT CTA CGG GCA TTG	622
Ile Asn Ile Ser Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu	

	195	200	205	
5	CAT TTA AGA GGT TAT GTG TTC CAG GAA CTC AGA GAA GAT GAT TTC CAG His Leu Arg Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Phe Gln 210 215 220	670		
10	CCC CTG ATG CAG CTT CCA AAC TTA TCG ACT ATC AAC TTG GGT ATT AAT Pro Leu Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn 225 230 235	718		
15	TTT ATT AAG CAA ATC GAT TTC AAA CTT TTC CAA AAT TTC TCC AAT CTG Phe Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu 240 245 250 255	766		
20	GAA ATT ATT TAC TTG TCA GAA AAC AGA ATA TCA CCG TTG GTA AAA GAT Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys Asp 260 265 270	814		
25	ACC CGG CAG AGT TAT GCA AAT AGT TCC TCT TTT CAA CGT CAT ATC CGG Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His Ile Arg 275 280 285	862		
30	AAA CGA CGC TCA ACA GAT TTT GAG TTT GAC CCA CAT TCG AAC TTT TAT Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser Asn Phe Tyr 290 295 300	910		
35	CAT TTC ACC CGT CCT TTA ATA AAG CCA CAA TGT GCT GCT TAT GGA AAA His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala Ala Tyr Gly Lys 305 310 315	958		
40	GCC TTA GAT TTA AGC CTC AAC AGT ATT TTC TT Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe 320 325	990		
	(2) INFORMATION FOR SEQ ID NO:16:			
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 329 amino acids			
	(B) TYPE: amino acid			
	(D) TOPOLOGY: linear			
	(ii) MOLECULE TYPE: protein			
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:			
	Asn Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys 1 5 10 15			
50	Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe 20 25 30			
	Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu 35 40 45			
55	Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu 50 55 60			
60	Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu 65 70 75 80			



(B) LOCATION: 1..513

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 278

(D) OTHER INFORMATION: /note= "nucleotide 278 designated G, may be G or C"

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 445

(D) OTHER INFORMATION: /note= "nucleotide 445 designated A, may be A or T"

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 572

(D) OTHER INFORMATION: /note= "nucleotides 572, 593, 600, 607, 617, 622, 625, 631, 640, 646, 653, 719, 775, and 861 are designated C; each may be A, C, G, or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

25	CAG TCT CTT TCC ACA TCC CAA ACT TTC TAT GAT GCT TAC ATT TCT TAT	48
	Gln Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr	
	1 5 10 15	
30	GAC ACC AAA GAT GCC TCT GTT ACT GAC TGG GTG ATA AAT GAG CTG CGC	96
	Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg	
	20 25 30	
35	TAC CAC CTT GAA GAG AGC CGA GAC AAA AAC GTT CTC CTT TGT CTA GAG	144
	Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu	
	35 40 45	
40	GAG AGG GAT TGG GAC CCG GGA TTG GCC ATC ATC GAC AAC CTC ATG CAG	192
	Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln	
	50 55 60	
45	AGC ATC AAC CAA AGC AAG AAA ACA GTA TTT GTT TTA ACC AAA AAA TAT	240
	Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr	
	65 70 75 80	
50	GCA AAA AGC TGG AAC TTT AAA ACA GCT TTT TAC TTG GGC TTG CAG AGG	288
	Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Gly Leu Gln Arg	
	85 90 95	
55	CTA ATG GGT GAG AAC ATG GAT GTG ATT ATA TTT ATC CTG CTG GAG CCA	336
	Leu Met Gly glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro	
	100 105 110	
60	GTG TTA CAG CAT TCT CCG TAT TTG AGG CTA CGG CAG CGG ATC TGT AAG	384
	Val Leu Gln His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys	
	115 120 125	
65	AGC TCC ATC CTC CAG TGG CCT GAC AAC CCG AAG GCA GAA AGG TTG TTT	432
	Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Arg Leu Phe	
	130 135 140	
70	TGG CAA ACT CTG AGA AAT GTG GTC TTG ACT GAA AAT GAT TCA CGG TAT	480

	Trp	Gln	Thr	Leu	Arg	Asn	Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	Arg	Tyr	
	145					150					155					160	
5	AAC	AAT	ATG	TAT	GTC	GAT	TCC	ATT	AAG	CAA	TAC	TAACTGACGT	TAAGTCATGA				533
	Asn	Asn	Met	Tyr	Val	Asp	Ser	Ile	Lys	Gln	Tyr						
					165					170							
	TTTCGCGCCA	TAATAAGAT	GCAAAGGAAT	GACATTTCCG	TATTAGTTAT	CTATTGCTAC											593
10	GGTAACCAA	TTACTCCAA	AAACCTTACG	TCGGTTTCAA	AACAACCACA	TTCTGCTGGC											653
	CCCACAGTTT	TTGAGGGTCA	GGAGTCCAGG	CCCAGCATAA	CTGGGTCTTC	TGCTTCAGGG											713
	TGTCTCCAGA	GGCTGCAATG	TAGGTGTTCA	CCAGAGACAT	AGGCATCACT	GCGGTCACAC											773
15	TCCATGTGGT	TGTTTTCTGG	ATTCAATTCC	TCCTGGGCTA	TTGGCCAAAG	GCTATACTCA											833
	TGTAAGCCAT	GCGAGCCTAT	CCCACAACGG	CAGCTTGCTT	CATCAGAGCT	AGCAAAAAAG											893
20	AGAGGTTGCT	AGCAAGATGA	AGTCACAATC	TTTTGTAAAT	GAATCAAAAA	AGTGATATCT											953
	CATCACTTTG	GCCATATTCT	ATTTGTTAGA	AGTAAACCAC	AGGTCCCACC	AGCTCCATGG											1013
	GAGTGACCAC	CTCACTCCAG	GGAAAACAGC	TGAAGACCAA	GATGGTGAGC	TCTGATTGCT											1073
25	TCAGTTGGTC	ATCAACTATT	TTCCCTTGAC	TGCTGTCCTG	GGATGGCCGG	CTATCTTGAT											1133
	GGATAGATTG	TGAATATCAG	GAGGCCAGGG	ATCACTGTGG	ACCATCTTAG	CAGTTGACCT											1193
30	AACACATCTT	CTTTTCAATA	TCTAAGAACT	TTTGCCACTG	TGACTAATGG	TCCTAATATT											1253
	AAGCTGTTGT	TTATATTTAT	CATATATCTA	TGGCTACATG	GTTATATTAT	GCTGTGGTTG											1313
	CGTTCGGTTT	TATTTACAGT	TGCTTTTACA	AATATTTGCT	GTAACATTTG	ACTTCTAAGG											1373
35	TTTAGATGCC	ATTTAAGAAC	TGAGATOGAT	AGCTTTTAA	GCATCTTTTA	CTTCTTACCA											1433
	TTTTTTAAAA	GTATGCAGCT	AAATTCGAAG	CTTTTGCTCT	ATATTGTAA	TTGCCATTGC											1493
40	TGTAATCTT	AAAATGAATG	AATAAAAATG	TTTCATTTTA	AAAAAAAAAA	AAAAAAAAAA											1553
	AAAA																1557

45 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

55

Gln	Ser	Leu	Ser	Thr	Ser	Gln	Thr	Phe	Tyr	Asp	Ala	Tyr	Ile	Ser	Tyr
1				5				10						15	

60

Asp	Thr	Lys	Asp	Ala	Ser	Val	Thr	Asp	Trp	Val	Ile	Asn	Glu	Leu	Arg
			20					25					30		



Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu  
 35 40 45  
 5 Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln  
 50 55 60  
 Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr  
 65 70 75 80  
 10 Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Gly Leu Gln Arg  
 85 90 95  
 Leu Met Gly Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro  
 100 105 110  
 15 Val Leu Gln His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys  
 115 120 125  
 Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Arg Leu Phe  
 130 135 140  
 20 Trp Gln Thr Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr  
 145 150 155 160  
 25 Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr  
 165 170

## (2) INFORMATION FOR SEQ ID NO:19:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 629 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: cDNA  
 (ix) FEATURE:  
 40 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..486  
 (ix) FEATURE:  
 45 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 144  
 (D) OTHER INFORMATION: /note= "nucleotides 144 and 225  
 designated C; may be C or T"

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAT GAA TTG ATC CCC AAT CTA GAG AAG GAA GAT GGT TCT ATC TTG ATT 48  
 Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp Gly Ser Ile Leu Ile  
 1 5 10 15  
 55 TGC CTT TAT GAA AGC TAC TTT GAC CCT GGC AAA AGC ATT AGT GAA AAT 96  
 Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn  
 20 25 30  
 60 ATT GTA AGC TTC ATT GAG AAA AGC TAT AAG TCC ATC TTT GTT TTG TCC 144  
 Ile Val Ser Phe Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser

	35		40		45	
5	CCC AAC TTT GTC CAG AAT GAG TGG TGC CAT TAT GAA TTC TAC TTT GCC Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala	192				
	50	55	60			
10	CAC CAC AAT CTC TTC CAT GAA AAT TCT GAT CAC ATA ATT CTT ATC TTA His His Asn Leu Phe His Glu Asn Ser Asp His Ile Ile Leu Ile Leu	240				
	65	70	75			
15	CTG GAA CCC ATT CCA TTC TAT TGC ATT CCC ACC AGG TAT CAT AAA CTG Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu	288				
	85	90	95			
20	GAA GCT CTC CTG GAA AAA AAA GCA TAC TTG GAA TGG CCC AAG GAT AGG Glu Ala Leu Leu Glu Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg	336				
	100	105	110			
25	CGT AAA TGT GGG CTT TTC TGG GCA AAC CTT CGA GCT GCT GTT AAT GTT Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Val Asn Val	384				
	115	120	125			
30	AAT GTA TTA GCC ACC AGA GAA ATG TAT GAA CTG CAG ACA TTC ACA GAG Asn Val Leu Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu	432				
	130	135	140			
35	TTA AAT GAA GAG TCT CGA GGT TCT ACA ATC TCT CTG ATG AGA ACA GAC Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp	480				
	145	150	155			
40	TGT CTA TAAATCCCA CAGTCCCTGG GAAGTTGGGG ACCACATACA CTGTTGGGAT Cys Leu	536				
35	GTACATTGAT ACAACCTTTA TGATGGCAAT TTGACAATAT TTATTAAAAAT AAAAAATGGT	596				
	TATTCCCTTC AAAAAAAAAA AAAAAAAAAA AAA	629				
40	(2) INFORMATION FOR SEQ ID NO:20:					
	(i) SEQUENCE CHARACTERISTICS:					
	(A) LENGTH: 162 amino acids					
	(B) TYPE: amino acid					
	(D) TOPOLOGY: linear					
45	(ii) MOLECULE TYPE: protein					
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:					
50	Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp Gly Ser Ile Leu Ile					
	1 5 10 15					
55	Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn					
	20 25 30					
	Ile Val Ser Phe Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser					
	35 40 45					
60	Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala					
	50 55 60					

His His Asn Leu Phe His Glu Asn Ser Asp His Ile Ile Leu Ile Leu  
 65 70 75 80  
 5 Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu  
 85 90 95  
 Glu Ala Leu Leu Glu Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg  
 100 105 110  
 10 Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Val Asn Val  
 115 120 125  
 Asn Val Leu Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu  
 130 135 140  
 15 Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp  
 145 150 155 160  
 20 Cys Leu

## (2) INFORMATION FOR SEQ ID NO:21:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 427 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 35 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

40 AAG AAC TCC AAA GAA AAC CTC CAG TTT CAT GCT TTT ATT TCA TAT AGT 48  
 Lys Asn Ser Lys Glu Asn Leu Gln Phe His Ala Phe Ile Ser Tyr Ser  
 1 5 10 15  
 45 GAA CAT GAT TCT GCC TGG GTG AAA AGT GAA TTG GTA CCT TAC CTA GAA 96  
 Glu His Asp Ser Ala Trp Val Lys Ser Glu Leu Val Pro Tyr Leu Glu  
 20 25 30  
 50 AAA GAA GAT ATA CAG ATT TGT CTT CAT GAG AGA AAC TTT GTC CCT GGC 144  
 Lys Glu Asp Ile Gln Ile Cys Leu His Glu Arg Asn Phe Val Pro Gly  
 35 40 45  
 55 AAG AGC ATT GTG GAA AAT ATC ATC AAC TGC ATT GAG AAG AGT TAC AAG 192  
 Lys Ser Ile Val Glu Asn Ile Ile Asn Cys Ile Glu Lys Ser Tyr Lys  
 50 55 60  
 TCC ATC TTT GTT TTG TCT CCC AAC TTT GTC CAG AGT GAG TGG TGC CAT 240  
 Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser Glu Trp Cys His  
 65 70 75 80  
 60 TAC GAA CTC TAT TTT GCC CAT CAC AAT CTC TTT CAT GAA GGA TCT AAT 288



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..627

10

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 54  
(D) OTHER INFORMATION: /note= "nucleotides 54, 103, and  
15 345 are designated A; each may be A or G"

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 313  
(D) OTHER INFORMATION: /note= "nucleotide 313 designated  
20 G, may be G or T"

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
25 (B) LOCATION: 316  
(D) OTHER INFORMATION: /note= "nucleotides 316, 380, 407,  
and 408 designated C; each may be A, C, G, or T"

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCT TCC ACC TGT GCC TGG CCT GGC TTC CCT GGC GGG GGC GGC AAA GTG	48
Ala Ser Thr Cys Ala Trp Pro Gly Phe Pro Gly Gly Gly Lys Val	
1 5 10 15	
35 GGC GAA ATG AGG ATG CCC TGC CCT ACG ATG CCT TCG TGG TCT TCG ACA	96
Gly Glu Met Arg Met Pro Cys Pro Thr Met Pro Ser Trp Ser Thr	
20 25 30	
40 AAA CGC AGA GCG CAG TGG CAG ACT GGG TGT ACA ACG AGC TTC GGG GGC	144
Lys Arg Arg Ala Gln Trp Gln Thr Gly Cys Thr Thr Ser Phe Gly Gly	
35 40 45	
45 AGC TGG AGG AGT GCC GTG GGC GCT GGG CAC TCC GCC TGT GCC TGG AGG	192
Ser Trp Arg Ser Ala Val Gly Ala Gly His Ser Ala Cys Ala Trp Arg	
50 55 60	
AAC GCG ACT GGC TGC CTG GCA AAA CCC TCT TTG AGA ACC TGT GGG CCT	240
Asn Ala Thr Gly Cys Leu Ala Lys Pro Ser Leu Arg Thr Cys Gly Pro	
65 70 75 80	
CGG TCT ATG GCA GCC GCA AGA CGC TGT TTG TGC TGG CCC ACA CGG ACC	288
Arg Ser Met Ala Ala Ala Arg Arg Cys Leu Cys Trp Pro Thr Arg Thr	
85 90 95	
55 GGG TCA GTG GTC TCT TGC GCG CCA GTT CTC CTG CTG GCC CAG CAG CGC	336
Gly Ser Val Val Ser Cys Ala Pro Val Leu Leu Leu Ala Gln Arg	
100 105 110	
60 CTG CTG GAA GAC CGC AAG GAC GTC GTG GTG CTG GTG ATC CTA ACG CCT	384
Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Thr Pro	

	115		120		125		
	GAC GGC CAA GCC TCC CGA CTA CCC GAT GCG CTG ACC AGC GCC TCT GCC						432
5	Asp Gly Gln Ala Ser Arg Leu Pro Asp Ala Leu Thr Ser Ala Ser Ala						
	130		135		140		
	GCC AGA GTG TCC TCC TCT GGC CCC ACC AGC CCA GTG GTC GCG CAG CTT						480
	Ala Arg Val Ser Ser Ser Gly Pro Thr Ser Pro Val Val Ala Gln Leu						
10	145		150		155		160
	CTG AGG CCA GCA TGC ATG GCC CTG ACC AGG GAC AAC CAC CAC TTC TAT						528
	Leu Arg Pro Ala Cys Met Ala Leu Thr Arg Asp Asn His His Phe Tyr						
	165		170		175		
15	AAC CGG AAC TTC TGC CAG GGA ACC CAC GGC CGA ATA GCC GTG AGC CGG						576
	Asn Arg Asn Phe Cys Gln Gly Thr His Gly Arg Ile Ala Val Ser Arg						
	180		185		190		
20	AAT CCT GCA CGG TGC CAC CTC CAC ACA CAC CTA ACA TAT GCC TGC CTG						624
	Asn Pro Ala Arg Cys His Leu His Thr His Leu Thr Tyr Ala Cys Leu						
	195		200		205		
	ATC TGACCAACAC ATGCTGCCA CCCTACCAC ACACC						662
25	Ile						

## (2) INFORMATION FOR SEQ ID NO:24:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 209 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

- 35 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

40	Ala Ser Thr Cys Ala Trp Pro Gly Phe Pro Gly Gly Gly Gly Lys Val		
	1	5	10
	Gly Glu Met Arg Met Pro Cys Pro Thr Met Pro Ser Trp Ser Ser Thr		
	20	25	30
45	Lys Arg Arg Ala Gln Trp Gln Thr Gly Cys Thr Thr Ser Phe Gly Gly		
	35	40	45
	Ser Trp Arg Ser Ala Val Gly Ala Gly His Ser Ala Cys Ala Trp Arg		
50	50	55	60
	Asn Ala Thr Gly Cys Leu Ala Lys Pro Ser Leu Arg Thr Cys Gly Pro		
	65	70	75
55	Arg Ser Met Ala Ala Ala Arg Arg Cys Leu Cys Trp Pro Thr Arg Thr		
	85	90	95
	Gly Ser Val Val Ser Cys Ala Pro Val Leu Leu Leu Ala Gln Gln Arg		
	100	105	110
60	Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Thr Pro		
	115	120	125

Asp Gly Gln Ala Ser Arg Leu Pro Asp Ala Leu Thr Ser Ala Ser Ala  
 130 135 140  
 5 Ala Arg Val Ser Ser Ser Gly Pro Thr Ser Pro Val Val Ala Gln Leu  
 145 150 155 160  
 Leu Arg Pro Ala Cys Met Ala Leu Thr Arg Asp Asn His His Phe Tyr  
 165 170 175  
 10 Asn Arg Asn Phe Cys Gln Gly Thr His Gly Arg Ile Ala Val Ser Arg  
 180 185 190  
 Asn Pro Ala Arg Cys His Leu His Thr His Leu Thr Tyr Ala Cys Leu  
 195 200 205  
 Ile  
 20 (2) INFORMATION FOR SEQ ID NO:25:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4865 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 30 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 107..2617  
 35 (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 173..2617  
 (ix) FEATURE:  
 40 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 81  
 (D) OTHER INFORMATION: /note= "nucleotides 81, 3144, 3205,  
 and 3563 designated A, each may be A, C, G, or T"  
 45 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 84  
 (D) OTHER INFORMATION: /note= "nucleotide 84 designated C,  
 may be C or G"  
 50 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 739  
 (D) OTHER INFORMATION: /note= "nucleotide 739 designated  
 55 C, may be C or T"  
 (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 3132  
 60 (D) OTHER INFORMATION: /note= "nucleotides 3132, 3532,  
 3538, and 3553 designated G, each may be G or T"

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 3638  
 (D) OTHER INFORMATION: /note= "nucleotide 3638 designated  
 A, may be A or T"

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 3677  
 (D) OTHER INFORMATION: /note= "nucleotides 3677, 3685, and  
 3736 designated C, each may be A or C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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AAAATACTCC CTGCTCTCAA AAACGCTCG GTCAAACGGT GATAGCAAAC CACGCATTCA      60
CAGGGCCACT GCTGCTCACA AAACCAGTGA GGATGATGCC AGGATG ATG TCT GCC      115
                                     Met Ser Ala
                                     -22   -20

TCG CGC CTG GCT GGG ACT CTG ATC CCA GCC ATG GCC TTC CTC TCC TGC      163
Ser Arg Leu Ala Gly Thr Leu Ile Pro Ala Met Ala Phe Leu Ser Cys
                    -15                -10                -5

GTG AGA CCA GAA AGC TGG GAG CCC TGC GTG GAG GTT CCT AAT ATT ACT      211
Val Arg Pro Glu Ser Trp Glu Pro Cys Val Glu Val Pro Asn Ile Thr
                        1                5                10

TAT CAA TGC ATG GAG CTG AAT TTC TAC AAA ATC CCC GAC AAC CTC CCC      259
Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp Asn Leu Pro
                    15                20                25

TTC TCA ACC AAG AAC CTG GAC CTG AGC TTT AAT CCC CTG AGG CAT TTA      307
Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu
                    30                35                40                45

GGC AGC TAT AGC TTC AGT TTC CCA GAA CTG CAG GTG CTG GAT TTA      355
Gly Ser Tyr Ser Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu
                        50                55                60

TCC AGG TGT GAA ATC CAG ACA ATT GAA GAT GGG GCA TAT CAG AGC CTA      403
Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu
                    65                70                75

AGC CAC CTC TCT ACC TTA ATA TTG ACA GGA AAC CCC ATC CAG AGT TTA      451
Ser His Leu Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu
                    80                85                90

GCC CTG GGA GCC TTT TCT GGA CTA TCA AGT TTA CAG AAG CTG GTG GCT      499
Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala
                    95                100                105

GTG GAG ACA AAT CTA GCA TCT CTA GAG AAC TTC CCC ATT GGA CAT CTC      547
Val Glu Thr Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu
                    110                115                120                125

AAA ACT TTG AAA GAA CTT AAT GTG GCT CAC AAT CTT ATC CAA TCT TTC      595
Lys Thr Leu Lys Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe
                    130                135                140

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5	AAA TTA CCT GAG TAT TTT TCT AAT CTG ACC AAT CTA GAG CAC TTG GAC Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp	643
	145 150 155	
10	CTT TCC AGC AAC AAG ATT CAA AGT ATT TAT TGC ACA GAC TTG CGG GTT Leu Ser Ser Ser Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val	691
	160 165 170	
15	CTA CAT CAA ATG CCC CTA CTC AAT CTC TCT TTA GAC CTG TCC CTG AAC Leu His Gln Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn	739
	175 180 185	
20	CCT ATG AAC TTT ATC CAA CCA GGT GCA TTT AAA GAA ATT AGG CTT CAT Pro Met Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His	787
	190 195 200 205	
25	AAG CTG ACT TTA AGA AAT AAT TTT GAT AGT TTA AAT GTA ATG AAA ACT Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr	835
	210 215 220	
30	TGT ATT CAA GGT CTG GCT GGT TTA GAA GTC CAT CGT TTG GTT CTG GGA Cys Ile Gln Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly	883
	225 230 235	
35	GAA TTT AGA AAT GAA GGA AAC TTG GAA AAG TTT GAC AAA TCT GCT CTA Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu	931
	240 245 250	
40	GAG GGC CTG TGC AAT TTG ACC ATT GAA GAA TTC CGA TTA GCA TAC TTA Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu	979
	255 260 265	
45	GAC TAC TAC CTC GAT GAT ATT ATT GAC TTA TTT AAT TGT TTG ACA AAT Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn	1027
	270 275 280 285	
50	GTT TCT TCA TTT TCC CTG GTG AGT GTG ACT ATT GAA AGG GTA AAA GAC Val Ser Ser Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp	1075
	290 295 300	
55	TTT TCT TAT AAT TTC GGA TGG CAA CAT TTA GAA TTA GTT AAC TGT AAA Phe Ser Tyr Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys	1123
	305 310 315	
60	TTT GGA CAG TTT CCC ACA TTG AAA CTC AAA TCT CTC AAA AGG CTT ACT Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr	1171
	320 325 330	
65	TTC ACT TCC AAC AAA GGT GGG AAT GCT TTT TCA GAA GTT GAT CTA CCA Phe Thr Ser Asn Lys Gly Asn Ala Phe Ser Ser Glu Val Asp Leu Pro	1219
	335 340 345	
70	AGC CTT GAG TTT CTA GAT CTC AGT AGA AAT GGC TTG AGT TTC AAA GGT Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly	1267
	350 355 360 365	
75	TGC TGT TCT CAA AGT GAT TTT GGG ACA ACC AGC CTA AAG TAT TTA GAT Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp	1315
	370 375 380	

	CTG AGC TTC AAT GGT GTT ATT ACC ATG AGT TCA AAC TTC TTG GGC TTA	1363
	Leu Ser Phe Asn Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu	
	385 390 395	
5	GAA CAA CTA GAA CAT CTG GAT TTC CAG CAT TCC AAT TTG AAA CAA ATG	1411
	Glu Gln Leu Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met	
	400 405 410	
10	AGT GAG TTT TCA GTA TTC CTA TCA CTC AGA AAC CTC ATT TAC CTT GAC	1459
	Ser Glu Phe Ser Val Phe Leu Ser Leu Arg Asn Leu Ile Tyr Leu Asp	
	415 420 425	
15	ATT TCT CAT ACT CAC ACC AGA GTT GCT TTC AAT GGC ATC TTC AAT GGC	1507
	Ile Ser His Thr His Arg Val Ala Phe Asn Gly Ile Phe Asn Gly	
	430 435 440 445	
20	TTG TCC AGT CTC GAA GTC TTG AAA ATG GCT GGC AAT TCT TTC CAG GAA	1555
	Leu Ser Ser Leu Glu Val Leu Lys Met Ala Gly Asn Ser Phe Gln Glu	
	450 455 460	
	AAC TTC CTT CCA GAT ATC TTC ACA GAG CTG AGA AAC TTG ACC TTC CTG	1603
	Asn Phe Leu Pro Asp Ile Phe Thr Glu Leu Arg Asn Leu Thr Phe Leu	
	465 470 475	
25	GAC CTC TCT CAG TGT CAA CTG GAG CAG TTG TCT CCA ACA GCA TTT AAC	1651
	Asp Leu Ser Ser Gln Cys Gln Leu Glu Gln Leu Ser Pro Thr Ala Phe Asn	
	480 485 490	
30	TCA CTC TCC AGT CTT CAG GTA CTA AAT ATG AGC CAC AAC AAC TTC TTT	1699
	Ser Leu Ser Ser Leu Gln Val Leu Asn Met Ser His Asn Asn Phe Phe	
	495 500 505	
35	TCA TTG GAT ACG TTT CCT TAT AAG TGT CTG AAC TCC CTC CAG GTT CTT	1747
	Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu Asn Ser Leu Gln Val Leu	
	510 515 520 525	
40	GAT TAC AGT CTC AAT CAC ATA ATG ACT TCC AAA CAG GAA CTA CAG	1795
	Asp Tyr Ser Leu Asn His Ile Met Thr Ser Lys Lys Gln Gln Leu Gln	
	530 535 540	
	CAT TTT CCA AGT AGT CTA GCT TTC TTA AAT CTT ACT CAG AAT GAC TTT	1843
	His Phe Pro Ser Ser Leu Ala Phe Leu Asn Leu Thr Gln Asn Asp Phe	
	545 550 555	
45	GCT TGT ACT TGT GAA CAC CAG AGT TTC CTG CAA TGG ATC AAG GAC CAG	1891
	Ala Cys Thr Cys Glu His Gln Ser Phe Leu Gln Trp Ile Lys Asp Gln	
	560 565 570	
50	AGG CAG CTC TTG GTG GAA GTT GAA CGA ATG GAA TGT GCA ACA CCT TCA	1939
	Arg Gln Leu Leu Val Glu Val Glu Arg Met Glu Cys Ala Thr Pro Ser	
	575 580 585	
55	GAT AAG CAG GGC ATG CCT GTG CTG AGT TTG AAT ATC ACC TGT CAG ATG	1987
	Asp Lys Gln Gly Met Pro Val Leu Ser Leu Asn Ile Thr Cys Gln Met	
	590 595 600 605	
60	AAT AAG ACC ATC ATT GGT GTG TCG GTC CTC AGT GTG CTT GTA GTA TCT	2035
	Asn Lys Thr Ile Ile Gly Val Ser Val Leu Ser Val Leu Val Val Ser	
	610 615 620	
	GTT GTA GCA GTT CTG GTC TAT AAG TTC TAT TTT CAC CTG ATG CTT CTT	2083

	Val	Val	Ala	Val	Leu	Val	Tyr	Lys	Phe	Tyr	Phe	His	Leu	Met	Leu	Leu		
			625						630					635				
5	GCT Ala	GGC Gly	TGC Cys 640	ATA Ile	AAG Lys	TAT Tyr	GGT Gly	AGA Arg 645	GGT Gly	GAA Glu	AAC Asn	ATC Ile	TAT Tyr 650	GAT Asp	GCC Ala	TTT Phe	2131	
	GTT Val	ATC Ile	TAC Tyr 655	TCA Ser	AGC Ser	CAG Gln	GAT Gln 660	GAG Glu	GAC Asp	TGG Trp	GTA Val	AGG Arg 665	AAT Asn	GAG Glu	CTA Leu	GTA Val	2179	
10	AAG Lys 670	AAT Asn	TTA Leu	GAA Glu	GAA Glu 675	GGG Gly	GTG Val	CCT Pro	CCA Pro	TTT Phe	CAG Gln 680	CTC Leu	TGC Cys	CTT Leu	CAC His	TAC Tyr 685	2227	
15	AGA Arg	GAC Asp	TTT Phe	ATT Ile	CCC Pro 690	GGT Gly	GTG Val	GCC Ala	ATT Ile	GCT Ala 695	GCC Ala	AAC Asn	ATC Ile	ATC Ile	CAT His 700	GAA Glu	2275	
20	GGT Gly	TTC Phe	CAT His	AAA Lys 705	AGC Ser	CGA Arg	AAG Lys	GTG Val	ATT Ile 710	GTT Val	GTG Val	GTG Val	TCC Ser	CAG Gln 715	CAC His	TTC Phe	2323	
25	ATC Ile	CAG Gln	AGC Ser 720	CGC Arg	TGG Trp	TGT Cys	ATC Ile	TTT Phe 725	GAA Glu	TAT Tyr	GAG Glu	ATT Ile	GCT Ala 730	CAG Gln	ACC Thr	TGG Trp	2371	
30	CAG Gln	TTT Phe 735	CTG Leu	AGC Ser	AGT Ser	CGT Arg	GCT Ala 740	GGT Gly	ATC Ile	ATC Ile	TTC Phe	ATT Ile 745	GTC Val	CTG Leu	CAG Gln	AAG Lys	2419	
35	GTG Val 750	GAG Glu	AAG Lys	ACC Thr	CTG Leu	CTC Leu 755	AGG Arg	CAG Gln	CAG Gln	GTG Val	GAG Glu 760	CTG Leu	TAC Tyr	CGC Arg	CTT Leu	CTC Leu 765	2467	
40	AGC Ser	AGG Arg	AAC Asn	ACT Thr	TAC Tyr 770	CTG Leu	GAG Glu	TGG Trp	GAG Glu	GAC Asp 775	AGT Ser	GTC Val	CTG Leu	GGG Gly	CGG Arg 780	CAC His	2515	
45	ATC Ile	TTC Phe	TGG Trp	AGA Arg 785	CGA Arg	CTC Leu	AGA Arg	AAA Lys	GCC Ala 790	CTG Leu	CTG Leu	GAT Asp	GGT Gly 795	AAA Lys	TCA Ser	TGG Trp	2563	
50	AAT Asn	CCA Pro	GAA Glu 800	GGA Gly	ACA Thr	GTG Val	GGT Gly	ACA Gly 805	GGA Cys	TGC Gln	AAT Asn	TGG Trp 810	CAG Gln	GAA Glu	GCA Ala	ACA Thr	2611	
	TCT Ser	ATC Ile 815	TGAAGAGGAA AAATAAAAC CTCCTGAGGC ATTTCTTGCC CAGCTGGGTC															2667
55	CAACACTTGT TCAGTTAATA AGTATTAAT GCTGCCACAT GTCAGGCCTT ATGCTAAGGG																	2727
	TGAGTAATTC CATGGTGCAC TAGATATGCA GGGCTGCTAA TCTCAAGGAG CTTCCAGTGC																	2787
	AGAGGGAATA AATGCTAGAC TAAATACAG AGTCTTCCAG GTGGGCATTT CAACCAACTC																	2847
60	AGTCAAGGAA CCCATGACAA AGAAAGTCAT TTCAACTCTT ACCTCATCAA GTTGAATAAA																	2907
	GACAGAGAAA ACAGAAAGAG ACATTTGTTCT TTTCTTGAGT CTTTGAATG GAAATTGTAT																	2967

	TATGTTATAG	CCATCATAAA	ACCATTTTGG	TAGTTTGTAC	TGAACTGGGT	GTTCACTTT	3027
	TCCTTTTGA	TTGAATACAA	TTTAAATTCT	ACTTGATGAC	TGCAGTCGTC	AAGGGGTCC	3087
5	TGATGCAAGA	TGCCCCTTCC	ATTTTAAGTC	TGTCCTTA	CAGAGSTTAA	AGTCTAATGG	3147
	CTAATTCCTA	AGGAAACCTG	ATTAACACAT	GCTCACAACC	ATCCTGGTCA	TTCTCGAACA	3207
10	TGTTCTATTT	TTTAACTAAT	CACCCCTGAT	ATATTTTTAT	TTTTATATAT	CCAGTTTTC	3267
	TTTTTTTACG	TCCTGCCTAT	AAGCTAATAT	CATAAATAAG	GTTGTTTAA	ACGTGCTTCA	3327
	AATATCCATA	TTAACCCTA	TTTTTCAAGG	AAGTATGGAA	AAGTACACTC	TGTCACCTTG	3387
15	TCACTCGATG	TCATTCCAAA	GTTATTGCCT	ACTAAGTAAT	GACTGTCATG	AAAGCAGCAT	3447
	TGAAATAATT	TGTTTAAAGG	GGGCACTCTT	TTAAACGGGA	AGAAAATTTC	CGCTTCCTGG	3507
20	TCTTATCATG	GACAAATTGG	GCTAGAGGCA	GGAAGGAAGT	GGGATGACCT	CAGGAAGTCA	3567
	CCTTTTCTTG	ATTCCAGAAA	CATATGGGCT	GATAAACCCG	GGGTGACCTC	ATGAAATGAG	3627
	TTGCAGCAGA	AGTTTATTTT	TTTCAGAAC	AGTGATGTTT	GATGGAACCT	TGAATCTCTT	3687
25	TAGGGAGACA	CAGATGGCTG	GGATCCCTCC	CCTGTACCCT	TCTCACTGCC	AGGAGAACTA	3747
	CGTGTGAAGG	TATTCAAGGC	AGGGAGTATA	CATTGCTGTT	TCCTGTTGGG	CAATGCTCCT	3807
	TGACCACATT	TTGGGAAGAG	TGGATGTTAT	CATTGAGAAA	ACAATGTGTC	TGGAATTAAT	3867
30	GGGGTCTCTA	TAAAGAAGGT	TCCCAGAAAA	GAATGTTTCA	TCCAGCTTCT	TCAGGAAACA	3927
	GGAACATTCA	AGGAAAAGGA	CAATCAGGAT	GTCATCAGGG	AAATGAAAAAT	AAAAACCACA	3987
35	ATGAGATATC	ACCTTATACC	AGGTAGATGG	CTACTATAAA	AAAATGAAGT	GTCATCAAGG	4047
	ATATAGAGAA	ATTGGAACCC	TTCTTCACTG	CTGGAGGGAA	TGGAAAAATG	TGTAGCCGTT	4107
40	ATGAAAAACA	GTACGGAGGT	TTCTCAAAAA	TTAAAAATAG	AATGCTATA	TGATCCAGCA	4167
	ATCTCACATC	TGTATATATA	CCCAAAATA	TTGAAATCAG	AATTTCAAGA	AAATATTTAC	4227
	ACTCCCATGT	TCATTGTGGC	ACTCTTCACA	ATCACTGTTT	CCAAAGTTAT	GGAAACAACC	4287
45	CAAATTTCCA	TTGAAAAATA	AATGGACAAA	GGAATGTGTC	ATATAACGTA	CAATGGGGAT	4347
	ATTATTCAGC	CTAAAAAAG	GGGGGATCCT	GTTATTTATG	ACAACATGAA	TAAACCCGGA	4407
50	GGCCATTATG	CTATGTAAAA	TGAGCAAGTA	ACAGAAAGAC	AAATACTGCC	TGATTTTCATT	4467
	TATATGAGGT	TCTAAAATAG	TCAAACCTCAT	AGAAGCAGAG	AATAGAACAG	TGGTTCCTAG	4527
	GGAAAAGGAG	GAAGGGAGAA	ATGAGGAAAT	AGGGAGTTGT	CTAATTGGTA	TAAAATTATA	4587
55	GTATGCAAGA	TGAATTAGCT	CTAAAGATCA	GCTGTATAGC	AGAGTTCGTA	TAATGAACAA	4647
	TACTGTATTA	TGCACTTAAC	ATTTTGTATA	GAGGTACCT	CTCATGTATA	GTGTTCTTAC	4707
	CATATACATA	TACACAAGGA	AGCTTTTGGG	GGTGATGGAT	ATATTTATTA	CCTTGATTGT	4767
60	GGTGATGGTT	TGACAGGTAT	GTGACTATGT	CTAAACCTCAT	CAAATGTAT	ACATTAAATA	4827

TATGCAGTTT TATAATATCA AAAAAAAAAA AAAAAAAAAA

4865

## 5 (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 837 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

15 Met Ser Ala Ser Arg Leu Ala Gly Thr Leu Ile Pro Ala Met Ala Phe  
 -22 -20 -15 -10

20 Leu Ser Cys Val Arg Pro Glu Ser Trp Glu Pro Cys Val Glu Val Pro  
 -5 1 5 10

Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp  
 15 20 25

25 Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu  
 30 35 40

Arg His Leu Gly Ser Tyr Ser Phe Ser Phe Pro Glu Leu Gln Val  
 45 50 55

30 Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr  
 60 65 70

35 Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile  
 75 80 85 90

Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys  
 95 100 105

40 Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile  
 110 115 120

Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His Asn Leu Ile  
 125 130 135

45 Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu  
 140 145 150

50 His Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp  
 155 160 165 170

Leu Arg Val Leu His Gln Met Pro Leu Leu Asn Leu Ser Leu Asp Leu  
 175 180 185

55 Ser Leu Asn Pro Met Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile  
 190 195 200

Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser Leu Asn Val  
 205 210 215

60 Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val His Arg Leu

	220		225		230	
	Val Leu Gly Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys					
	235		240		245	250
5	Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu					
		255				265
10	Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys					
		270		275		280
	Leu Thr Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr Ile Glu Arg					
		285		290		295
15	Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp Gln His Leu Glu Leu Val					
		300		305		310
	Asn Cys Lys Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys					
		315		320		325
20	Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe Ser Glu Val					
			335		340	345
25	Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser					
		350		355		360
	Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys					
		365		370		375
30	Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile Thr Met Ser Ser Asn Phe					
		380		385		390
	Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His Ser Asn Leu					
		395		400		405
35	Lys Gln Met Ser Glu Phe Ser Val Phe Leu Ser Leu Arg Asn Leu Ile					
			415		420	425
40	Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe Asn Gly Ile					
		430		435		440
	Phe Asn Gly Leu Ser Ser Leu Glu Val Leu Lys Met Ala Gly Asn Ser					
		445		450		455
45	Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Glu Leu Arg Asn Leu					
		460		465		470
	Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu Ser Pro Thr					
		475		480		485
50	Ala Phe Asn Ser Leu Ser Ser Leu Gln Val Leu Asn Met Ser His Asn					
			495		500	505
	Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu Asn Ser Leu					
		510		515		520
	Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser Lys Lys Gln					
		525		530		535
60	Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn Leu Thr Gln					
		540		545		550

Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu Gln Trp Ile  
 555 560 565 570  
 5 Lys Asp Gln Arg Gln Leu Leu Val Glu Val Glu Arg Met Glu Cys Ala  
 575 580 585  
 Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu Asn Ile Thr  
 590 595 600  
 10 Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Leu Ser Val Leu  
 605 610 615  
 Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr Phe His Leu  
 620 625 630  
 15 Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu Asn Ile Tyr  
 635 640 645 650  
 20 Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp Val Arg Asn  
 655 660 665  
 Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe Gln Leu Cys  
 670 675 680  
 25 Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Asn Ile  
 685 690 695  
 Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val Val Val Ser  
 700 705 710  
 Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala  
 715 720 725 730  
 35 Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile Phe Ile Val  
 735 740 745  
 Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu Leu Tyr  
 750 755 760  
 40 Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu  
 765 770 775  
 Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly  
 780 785 790  
 45 Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys Asn Trp Gln  
 795 800 805 810  
 50 Glu Ala Thr Ser Ile  
 815

## (2) INFORMATION FOR SEQ ID NO:27:

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 60 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..300

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 186  
 (D) OTHER INFORMATION: /note= "nucleotides 186, 196, 217, 276, and 300 designated C, each may be A, C, G, or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

15	TCC TAT TCT ATG GAA AAA GAT GCT TTC CTA TTT ATG AGA AAT TTG AAG	48
	Ser Tyr Ser Met Glu Lys Asp Ala Phe Leu Phe Met Arg Asn Leu Lys	
	1 5 10 15	
20	GTT CTC TCA CTA AAA GAT AAC AAT GTC ACA GCT GTC CCC ACC ACT TTG	96
	Val Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu	
	20 25 30	
25	CCA CCT AAT TTA CTA GAG CTC TAT CTT TAT AAC AAT ATC ATT AAG AAA	144
	Pro Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys	
	35 40 45	
30	ATC CAA GAA AAT GAT TTC AAT AAC CTC AAT GAG TTG CAA GTC CTT GAC	192
	Ile Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Val Leu Asp	
	50 55 60	
35	CTA CGT GGA AAT TGC CCT CGA TGT CAT AAT GTC CCA TAT CCG TGT ACA	240
	Leu Arg Gly Asn Cys Pro Arg Cys His Asn Val Pro Tyr Pro Cys Thr	
	65 70 75 80	
40	CCG TGT GAA AAT AAT TCC CCC TTA CAG ATC CAT GAC AAT GCT TTC AAT	288
	Pro Cys Glu Asn Asn Ser Pro Leu Gln Ile His Asp Asn Ala Phe Asn	
	85 90 95	
45	TCA TCG ACA GAC	300
	Ser Ser Thr Asp	
	100	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

55	Ser Tyr Ser Met Glu Lys Asp Ala Phe Leu Phe Met Arg Asn Leu Lys
	1 5 10 15
60	Val Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu
	20 25 30



Pro Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys  
                   35                                  40                                  45

5 Ile Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Val Leu Asp  
                   50                                  55                                  60

Leu Arg Gly Asn Cys Pro Arg Cys His Asn Val Pro Tyr Pro Cys Thr  
                   65                                  70                                  75                                  80

10 Pro Cys Glu Asn Asn Ser Pro Leu Gln Ile His Asp Asn Ala Phe Asn.  
                                   85                                  90                                  95

Ser Ser Thr Asp  
                   100

15

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1756 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

25

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1182

30

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1643  
 (D) OTHER INFORMATION: /note= "nucleotide 1643 designated

35

A, may be A or G"

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1664  
 (D) OTHER INFORMATION: /note= "nucleotide 1664 designated

40

C, may be A, C, G, or T"

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1680  
 (D) OTHER INFORMATION: /note= "nucleotides 1680 and 1735

45

designated G, may be G or T"

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1719  
 (D) OTHER INFORMATION: /note= "nucleotide 1719 designated

50

C, may be C or T"

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1727  
 (D) OTHER INFORMATION: /note= "nucleotide 1727 designated

55

A, may be A, G, or T"

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

5	TCT CCA GAA ATT CCC TGG AAT TCC TTG CCT CTT GAG GTT TTT GAG GGT Ser Pro Glu Ile 5 Trp Asn Ser Leu Pro Pro Glu Val Phe Glu Gly 15	48
10	ATG CCG CCA AAT CTA AAG AAT CTC TCC TTG GCC AAA AAT GGG CTC AAA Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys 20 25 30	96
15	TCT TTC TTT TGG GAC AGA CTC CAG TTA CTG AAG CAT TTG GAA ATT TTG Ser Phe Phe Trp Asp Arg Leu Leu Leu Lys His Leu Glu Ile Leu 35 40 45	144
20	GAC CTC AGC CAT AAC CAG CTG ACA AAA GTA CCT GAG AGA TTG GCC AAC Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala Asn 50 55 60	192
25	TGT TCC AAA AGT CTC ACA ACA CTG ATT CTT AAG CAT AAT CAA ATC AGG Cys Ser Lys Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile Arg 65 70 75 80	240
30	CAA TTG ACA AAA TAT TTT CTA GAA GAT GCT TTG CAA TTG CGC TAT CTA Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr Leu 85 90 95	288
35	GAC ATC AGT TCA AAT AAA ATC CAG GTC ATT CAG AAG ACT AGC TTC CCA Asp Ile Ser 100 Trp Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe Pro 105 110	336
40	GAA AAT GTC CTC AAC AAT CTG GAG ATG TTG GTT TTA CAT CAC AAT CGC Glu Asn Val Leu Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn Arg 115 120 125	384
45	TTT CTT TGC AAC TGT GAT GCT GTG TGG TTT GTC TGG TGG GTT AAC CAT Phe Leu Cys Asn Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His 130 135 140	432
50	ACA GAT GTT ACT ATT CCA TAC CTG GCC ACT GAT GTG ACT TGT GTA GGT Thr Asp Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly 145 150 155 160	480
55	CCA GGA GCA CAC AAA GGT CAA AGT GTC ATA TCC CTT GAT CTG TAT ACG Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr 165 170 175	528
60	TGT GAG TTA GAT CTC ACA AAC CTG ATT CTG TTC TCA GTT TCC ATA TCA Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile Ser 180 185 190	576
65	TCA GTC CTC TTT CTT ATG GTA GTT ATG ACA ACA AGT CAC CTC TTT TTC Ser Val Leu Phe Leu Met Val Val Met Thr Thr Ser His Leu Phe Phe 195 200 205	624
70	TGG GAT ATG TGG TAC ATT TAT TAT TTT TGG AAA GCA AAG ATA AAG GGG Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys Gly 210 215 220	672
75	TAT CCA GCA TCT GCA ATC CCA TGG AGT CCT TGT TAT GAT GCT TTT ATT Tyr Pro Ala Ser Ala Ile Pro Trp Ser Pro Cys Tyr Asp Ala Phe Ile 225 230 235 240	720

	GTG TAT GAC ACT AAA AAC TCA GCT GTG ACA GAA TGG GTT TTG CAG GAG	768
	Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu	
	245 250 255	
5	CTG GTG GCA AAA TTG GAA GAT CCA AGA GAA AAA CAC TTC AAT TTG TGT	816
	Leu Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys	
	260 265 270	
10	CTA GAA GAA AGA GAC TGG CTA CCA GGA CAG CCA GTT CTA GAA AAC CTT	864
	Leu Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu	
	275 280 285	
15	TCC CAG AGC ATA CAG CTC AGC AAA AAG ACA GTG TTT GTG ATG ACA CAG	912
	Ser Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Gln	
	290 295 300	
	AAA TAT GCT AAG ACT GAG AGT TTT AAG ATG GCA TTT TAT TTG TCT CAT	960
	Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His	
	305 310 315 320	
20	CAG AGG CTC CTG GAT GAA AAA GTG GAT GTG ATT ATC TTG ATA TTC TTG	1008
	Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu	
	325 330 335	
25	GAA AGA CCT CTT CAG AAG TCT AAG TTT CTT CAG CTC AGG AAG AGA CTC	1056
	Glu Arg Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu	
	340 345 350	
30	TGC AGG AGC TCT GTC CTT GAG TGG CCT GCA AAT CCA CAG GCT CAC CCA	1104
	Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His Pro	
	355 360 365	
35	TAC TTC TGG CAG TGC CTG AAA AAT GCC CTG ACC ACA GAC AAT CAT GTG	1152
	Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn His Val	
	370 375 380	
	GCT TAT AGT CAA ATG TTC AAG GAA ACA GTC TAGCTCTCTG AAGAATGTCA	1202
	Ala Tyr Ser Gln Met Phe Lys Glu Thr Val	
	385 390	
40	CCACCTAGGA CATGCCTTGG TACCTGAAGT TTTCATAAAG GTTTCACATA ATGAAGGTCT	1262
45	GAATTTTTC TAACAGTTGT CATGGCTCAG ATTGGTGGGA AATCATCAAT ATATGGCTAA	1322
	GAAATTAAGA AGGGGAGACT GATAGAAGAT AATTTCITTC TTCATGTGCC ATGCTCAGTT	1382
	AAATATTTCC CCTAGCTCAA ATCTGAAAAA CTGTGCCTAG GAGACAACAC AAGGCTTTGA	1442
50	TTTATCTGCA TACAATTGAT AAGAGCCACA CATCTGCCCT GAAGAAGTAC TAGTAGTTTT	1502
	AGTAGTAGGG TAAAAATTAC ACAAGCTTTC TCTCTCTCTG ATACTGAACT GTACCAGAGT	1562
55	TCAATGAAAT AAAAGCCACAG AGAACTTCTC AGTAAATGGT TTCATTATCA TGATGATACC	1622
	ACCATGCAAT ATGCCACAAA ACCGCTACTG GTACAGGACA GCTGGTAGCT GCTTCAAGGC	1682
	CTCTTATCAT TTTCITGGGG CCCATGGAGG GGTTCTCTGG GAAAAAGGGA AGGTTTTTTT	1742
60	TGGCCATCCA TGAA	1756

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 394 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Pro Glu Ile Pro Trp Asn Ser Leu Pro Pro Glu Val Phe Glu Gly  
 1 5 10 15  
 Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys  
 20 25 30  
 Ser Phe Phe Trp Asp Arg Leu Gln Leu Leu Lys His Leu Glu Ile Leu  
 35 40 45  
 Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala Asn  
 50 55 60  
 Cys Ser Lys Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile Arg  
 65 70 75 80  
 Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr Leu  
 85 90 95  
 Asp Ile Ser Ser Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe Pro  
 100 105 110  
 Glu Asn Val Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn Arg  
 115 120 125  
 Phe Leu Cys Asn Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His  
 130 135 140  
 Thr Asp Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly  
 145 150 155 160  
 Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr  
 165 170 175  
 Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile Ser  
 180 185 190  
 Ser Val Leu Phe Leu Met Val Val Met Thr Thr Ser His Leu Phe Phe  
 195 200 205  
 Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys Gly  
 210 215 220  
 Tyr Pro Ala Ser Ala Ile Pro Trp Ser Pro Cys Tyr Asp Ala Phe Ile  
 225 230 235 240  
 Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu  
 245 250 255  
 Leu Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys

[illegible]

(2) INFORMATION FOR SEO ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 2..847

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: 4  
(D) OTHER INFORMATION: /note= "nucleotides 4 and 23  
ed C, each may be A, C, G, or T"

(ix) FEATURE:

- ```

      (A) NAME/KEY: misc_feature
      (B) LOCATION: 650
      (D) OTHER INFORMATION: /note= "nucleotide 650 designated
G, may be A or G"

```

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: 715  
(D) OTHER INFORMATION: /note= "nucleotides 715, 825, and 845 designated C, each may be C or T"

(xi) SEQUENCE DESCRIPTION: SEO ID NO:31:

|    |                                                                 |     |
|----|-----------------------------------------------------------------|-----|
|    | C TCC GAT GCC AAG ATT CGG CAC CAG GCA TAT TCA GAG GTC ATG ATG   | 46  |
|    | Ser Asp Ala Lys Ile Arg His Gln Ala Tyr Ser Glu Val Met Met     |     |
|    | 1 5 10 15                                                       |     |
| 5  | GTT GGA TGG TCA GAT TCA TAC ACC TGT GAA TAC CCT TTA AAC CTA AGG | 94  |
|    | Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg |     |
|    | 20 25 30                                                        |     |
| 10 | GGA ACT AGG TTA AAA GAC GTT CAT CTC CAC GAA TTA TCT TGC AAC ACA | 142 |
|    | Gly Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr |     |
|    | 35 40 45                                                        |     |
| 15 | GCT CTG TTG ATT GTC ACC ATT GTG GTT ATT ATG CTA GTT CTG GGG TTG | 190 |
|    | Ala Leu Leu Ile Val Thr Ile Val Ile Met Leu Val Leu Gly Leu     |     |
|    | 50 55 60                                                        |     |
| 20 | GCT GTG GCC TTC TGC TGT CTC CAC TTT GAT CTG CCC TGG TAT CTC AGG | 238 |
|    | Ala Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg |     |
|    | 65 70 75                                                        |     |
| 25 | ATG CTA GGT CAA TGC ACA CAA ACA TGG CAC AGG GTT AGG AAA ACA ACC | 286 |
|    | Met Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr |     |
|    | 80 85 90 95                                                     |     |
| 30 | CAA GAA CAA CTC AAG AGA AAT GTC CGA TTC CAC GCA TTT ATT TCA TAC | 334 |
|    | Gln Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr |     |
|    | 100 105 110                                                     |     |
| 35 | AGT GAA CAT GAT TCT CTG TGG GTG AAG AAT GAA TTG ATC CCC AAT CTA | 382 |
|    | Ser Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu |     |
|    | 115 120 125                                                     |     |
| 40 | GAG AAG GAA GAT GGT TCT ATC TTG ATT TGC CTT TAT GAA AGC TAC TTT | 430 |
|    | Glu Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe |     |
|    | 130 135 140                                                     |     |
| 45 | GAC CCT GGC AAA AGC ATT AGT GAA AAT ATT GTA AGC TTC ATT GAG AAA | 478 |
|    | Asp Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys |     |
|    | 145 150 155                                                     |     |
| 50 | AGC TAT AAG TCC ATC TTT GTT TTG TCT CCC AAC TTT GTC CAG AAT GAG | 526 |
|    | Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu |     |
|    | 160 165 170 175                                                 |     |
| 55 | TGG TGC CAT TAT GAA TTC TAC TTT GCC CAC CAC AAT CTC TTC CAT GAA | 574 |
|    | Trp Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu |     |
|    | 180 185 190                                                     |     |
| 60 | AAT TCT GAT CAC ATA ATT CTT ATC TTA CTG GAA CCC ATT CCA TTC TAT | 622 |
|    | Asn Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr |     |
|    | 195 200 205                                                     |     |
| 65 | TGC ATT CCC ACC AGG TAT CAT AAA CTG GAA GCT CTC CTG GAA AAA AAA | 670 |
|    | Cys Ile Pro Thr Arg Tyr His Lys Leu Glu Ala Leu Leu Glu Lys Lys |     |
|    | 210 215 220                                                     |     |
| 70 | GCA TAC TTG GAA TGG CCC AAG GAT AGG CGT AAA TGT GGG CTT TTC TGG | 718 |
|    | Ala Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Phe Trp |     |
|    | 225 230 235                                                     |     |

GCA AAC CTT CGA GCT GCT GTT AAT GTT AAT GTA TTA GCC ACC AGA GAA 766  
Ala Asn Leu Arg Ala Ala Val Asn Val Asn Val Leu Ala Thr Arg Glu  
240 245 250 255

5 ATG TAT GAA CTG CAG ACA TTC ACA GAG TTA AAT GAA GAG TCT CGA GGT 814  
Met Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly  
260 265 270

10 TCT ACA ATC TCT CTG ATG AGA ACA GAC TGT CTA TAAATCCCA CAGTCCTTGG 867  
Ser Thr Ile Ser Leu Met Arg Thr Asp Cys Leu  
275 280

GAAGTTGGGG ACCACATACA CTGTTGGGAT GTACATTGAT ACAACCTTTA TGATGGCAAT 927

15 TTGACAATAT TTATTAATAA AAAAATGGT TATTCCTTC AAAAAAAAAA AAAAAAAAAA 987  
AAAAAAAAAA AA 999

20 (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 282 amino acids  
(B) TYPE: amino acid  
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

30 Ser Asp Ala Lys Ile Arg His Gln Ala Tyr Ser Glu Val Met Met Val  
1 5 10 15

35 Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly  
20 25 30

Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr Ala  
35 40 45

40 Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu Ala  
50 55 60

Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg Met  
65 70 75 80

45 Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln  
85 90 95

50 Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser  
100 105 110

Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu  
115 120 125

55 Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp  
130 135 140

Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser  
145 150 155 160

60 Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp

165 170 175

Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu Asn  
180 185 190

5 Ser Asp His Ile Ile Leu Ile Leu Glu Pro Ile Pro Phe Tyr Cys  
195 200 205

Ile Pro Thr Arg Tyr His Lys Leu Glu Ala Leu Leu Glu Lys Lys Ala  
210 215 220

10 Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Phe Trp Ala  
225 230 235 240

15 Asn Leu Arg Ala Ala Val Asn Val Asn Val Leu Ala Thr Arg Glu Met  
245 250 255

Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser  
260 265 270

20 Thr Ile Ser Leu Met Arg Thr Asp Cys Leu  
275 280

(2) INFORMATION FOR SEQ ID NO:33:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..1008

40 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 854  
(D) OTHER INFORMATION: /note= "nucleotide 854 designated  
A, may be A or T"

45 (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1171  
(D) OTHER INFORMATION: /note= "nucleotides 1171 and 1172  
designated C, each may be A, C, G, or T"

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTG CCT GCT GGC ACC CGG CTC CGG AGG CTG GAT GTC AGC TGC AAC AGC  
Leu Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser  
1 5 10 15

ATC AGC TTC GTG GCC CCC GGC TTC TTT TCC AAG GCC AAG GAG CTG CGA  
Ile Ser Phe Val Ala Pro Gly Phe Phe Ser Lys Ala Lys Glu Leu Arg  
20 25 30

48 96



|    |                                                                 |     |
|----|-----------------------------------------------------------------|-----|
|    | GAG CTC AAC CTT AGC GCC AAC GCC CTC AAG ACA GTG GAC CAC TCC TGG | 144 |
|    | Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp |     |
|    | 35 40 45                                                        |     |
| 5  | TTT GGG CCC CTG GCG AGT GCC CTG CAA ATA CTA GAT GTA AGC GCC AAC | 192 |
|    | Phe Gly Pro Leu Ala Ser Ala Leu Gln Ile Leu Asp Val Ser Ala Asn |     |
|    | 50 55 60                                                        |     |
| 10 | CCT CTG CAC TGC GCC TGT GGG GCG GCC TTT ATG GAC TTC CTG CTG GAG | 240 |
|    | Pro Leu His Cys Ala Cys Gly Ala Ala Phe Met Asp Phe Leu Leu Glu |     |
|    | 65 70 75 80                                                     |     |
| 15 | GTG CAG GCT GCC GTG CCC GGT CTG CCC AGC CGG GTG AAG TGT GGC AGT | 288 |
|    | Val Gln Ala Ala Val Pro Gly Leu Pro Ser Arg Val Lys Cys Gly Ser |     |
|    | 85 90 95                                                        |     |
| 20 | CCG GGC CAG CTC CAG GGC CTC AGC ATC TTT GCA CAG GAC CTG CGC CTC | 336 |
|    | Pro Gly Gln Leu Gln Gly Leu Ser Ile Phe Ala Gln Asp Gly Arg Leu |     |
|    | 100 105 110                                                     |     |
|    | TGC CTG GAT GAG GCC CTC TCC TGG GAC TGT TTC GCC CTC TCG CTG CTG | 384 |
|    | Cys Leu Asp Glu Ala Leu Ser Trp Asp Cys Phe Ala Leu Ser Leu Leu |     |
|    | 115 120 125                                                     |     |
| 25 | GCT GTG GCT CTG GGC CTG GGT GTG CCC ATG CTG CAT CAC CTC TGT GGC | 432 |
|    | Ala Val Ala Leu Gly Leu Gly Val Pro Met Leu His His Leu Cys Gly |     |
|    | 130 135 140                                                     |     |
| 30 | TGG GAC CTC TGG TAC TGC TTC CAC CTG TGC CTG GCC TGG CTT CCC TGG | 480 |
|    | Trp Asp Leu Trp Tyr Cys Phe His Leu Cys Leu Ala Trp Leu Pro Trp |     |
|    | 145 150 155 160                                                 |     |
| 35 | CGG GGG CGG CAA AGT GGG CGA GAT GAG GAT GCC CTG CCC TAC GAT GCC | 528 |
|    | Arg Gly Arg Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala |     |
|    | 165 170 175                                                     |     |
| 40 | TTC CTG GTC TTC GAC AAA ACG CAG AGC GCA GTG GCA GAC TGG GTG TAC | 576 |
|    | Phe Val Val Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr |     |
|    | 180 185 190                                                     |     |
|    | AAC GAG CTT CGG GGG CAG CTG GAG GAG TGC CGT GGG CGC TGG GCA CTC | 624 |
|    | Asn Glu Leu Arg Gly Gln Leu Glu Glu Cys Arg Gly Arg Trp Ala Leu |     |
|    | 195 200 205                                                     |     |
| 45 | CGC CTG TGC CTG GAG GAA CGC GAC TGG CTG CCT GGC AAA ACC CTC TTT | 672 |
|    | Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe |     |
|    | 210 215 220                                                     |     |
| 50 | GAG AAC CTG TGG GCC TCG GTC TAT GGC AGC CGC AAG ACG CTG TTT GTG | 720 |
|    | Glu Asn Leu Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val |     |
|    | 225 230 235 240                                                 |     |
| 55 | CTG GCC CAC ACG GAC CGG GTC AGT GGT CTC TTG CGC GCC AGC TTC CTG | 768 |
|    | Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu |     |
|    | 245 250 255                                                     |     |
| 60 | CTG GCC CAG CAG CGC CTG CTG GAG GAC CGC AAG GAC GTC GTG GTG CTG | 816 |
|    | Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu |     |
|    | 260 265 270                                                     |     |
|    | GTG ATC CTG AGC CCT GAC GGC CGC CGC TCC CGC TAC GAG CGG CTG CGC | 864 |

|    |                                                                                                                                       |              |
|----|---------------------------------------------------------------------------------------------------------------------------------------|--------------|
|    | Val Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Glu Arg Leu Arg                                                                       |              |
|    | 275 280 285                                                                                                                           |              |
| 5  | CAG CGC CTC TGC CGC CAG AGT GTC CTC CTC TGG CCC CAC CAG CCC AGT<br>Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser    | 912          |
|    | 290 295 300                                                                                                                           |              |
| 10 | GGT CAG CGC AGC TTC TGG GCC CAG CTG GGC ATG GCC CTG ACC AGG GAC<br>Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp    | 960          |
|    | 305 310 315 320                                                                                                                       |              |
| 15 | AAC CAC CAC TTC TAT AAC CGG AAC TTC TGC CAG GGA CCC ACG GCC GAA<br>Asn His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu    | 1008         |
|    | 325 330 335                                                                                                                           |              |
| 20 | TAGCCGTGAG CCGGAATCCT GCACGGTGCC ACCTCCACAC TCACCTCACC TCTGCCTGCC<br>TGCTCTGACC CTCCCCTGCT GCCTCCCTC ACCCCACACC TGACACAGAG CAGGCACTCA | 1068<br>1128 |
|    | ATAAATGCTA CCGAAGCTA AAAAAAAAAA AAAAAAAAAA AACCA                                                                                      | 1173         |

(2) INFORMATION FOR SEQ ID NO:34:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

|    |                                                                 |  |
|----|-----------------------------------------------------------------|--|
| 35 | Leu Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser |  |
|    | 1 5 10 15                                                       |  |
|    | Ile Ser Phe Val Ala Pro Gly Phe Ser Lys Ala Lys Glu Leu Arg     |  |
|    | 20 25 30                                                        |  |
| 40 | Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp |  |
|    | 35 40 45                                                        |  |
|    | Phe Gly Pro Leu Ala Ser Ala Leu Gln Ile Leu Asp Val Ser Ala Asn |  |
|    | 50 55 60                                                        |  |
| 45 | Pro Leu His Cys Ala Cys Gly Ala Ala Phe Met Asp Phe Leu Leu Glu |  |
|    | 65 70 75 80                                                     |  |
| 50 | Val Gln Ala Ala Val Pro Gly Leu Pro Ser Arg Val Lys Cys Gly Ser |  |
|    | 85 90 95                                                        |  |
|    | Pro Gly Gln Leu Gln Gly Leu Ser Ile Phe Ala Gln Asp Leu Arg Leu |  |
|    | 100 105 110                                                     |  |
| 55 | Cys Leu Asp Glu Ala Leu Ser Trp Asp Cys Phe Ala Leu Ser Leu Leu |  |
|    | 115 120 125                                                     |  |
|    | Ala Val Ala Leu Gly Leu Gly Val Pro Met Leu His His Leu Cys Gly |  |
|    | 130 135 140                                                     |  |
| 60 | Trp Asp Leu Trp Tyr Cys Phe His Leu Cys Leu Ala Trp Leu Pro Trp |  |

145                      150                      155                      160  
 Arg Gly Arg Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala  
 165                      170                      175  
 5 Phe Val Val Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr  
 180                      185                      190  
 10 Asn Glu Leu Arg Gly Gln Leu Glu Cys Arg Gly Arg Trp Ala Leu  
 195                      200                      205  
 Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe  
 210                      215                      220  
 15 Glu Asn Leu Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val  
 225                      230                      235                      240  
 Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu  
 245                      250                      255  
 20 Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu  
 260                      265                      270  
 25 Val Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Glu Arg Leu Arg  
 275                      280                      285  
 Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser  
 290                      295                      300  
 30 Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp  
 305                      310                      315                      320  
 Asn His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu  
 325                      330                      335  
 35

## (2) INFORMATION FOR SEQ ID NO:35:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 497 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: cDNA

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGGCCACAC GGACCGGTC AGTGGCCTCC TGGCACCAGC CTTCCTGCTG GCTCAGCAGC 60  
 GCCTGTGGGA AGACCGCAAG GACGTGGTGG TGTGTGTGAT CCTGCGTCCG GATGCCCCAC 120  
 55 CGTCCCCTGA TGTGCGACTG CGCCAGCGTC TCTGCCGCCA GAGTGTGCTC TTCTGGCCCC 180  
 AGCGACCCAA CGGGCAGGGG GGCTTCTGGG CCCAGCTGAG TACAGCCCTG ACTAGGGACA 240  
 60 ACCGCCACTT CTATAACCAG AACTTCTGCC GGGGACCTAC AGCAGAATAG CTCAGAGCAA 300

|              |            |            |            |            |             |     |
|--------------|------------|------------|------------|------------|-------------|-----|
| CAGCTGGAAA   | CAGCTGCATC | TTCATGTCTG | GTCCCCGAGT | TGCTCTGCCT | GCC'TTGCTCT | 360 |
| GTCTTACTAC   | ACCGCTATTT | GGCAAGTGC  | CAATATATGC | TACCAAGCCA | CCAGGCCAC   | 420 |
| 5 GGAGCAAAGG | TTGGCTGTAA | AGGGTAGTTT | TCTTCCCATG | CATCTTTCAG | GAGAGTGAAG  | 480 |
| ATAGACACCA   | AACCCAC    |            |            |            |             | 497 |

## WHAT IS CLAIMED IS:

1. A substantially pure or recombinant DTLR2 protein or peptide which exhibits at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 4.
2. A substantially pure or recombinant DTLR3 protein or peptide which exhibits at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 6.
3. A substantially pure or recombinant DTLR4 protein or peptide which exhibits at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 26.
4. A substantially pure or recombinant DTLR5 protein or peptide which exhibits at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 10.
5. A substantially pure or recombinant DTLR6 protein or peptide which exhibits at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 12.
6. A substantially pure or recombinant DTLR7 protein or peptide which exhibits at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 16 or 18.
7. A substantially pure or recombinant DTLR8 protein or peptide which exhibits at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 32.

8. A substantially pure or recombinant DTLR9 protein or peptide which exhibits at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 22.

5

9. A substantially pure or recombinant DTLR10 protein or peptide which exhibits at least about 85% sequence identity over a length of at least about 12 amino acids to SEQ ID NO: 34.

10

10. A fusion protein comprising the protein or peptide of any of claims 1-9.

11. A binding compound which specifically binds to the protein or peptide of any of claims 1-9.

12. The binding compound of claim 11 which is an antibody or antibody fragment.

13. A nucleic acid encoding the protein or peptide of any of claims 1-9.

14. An expression vector comprising the nucleic acid of claim 13.

25

15. A host cell comprising the vector of claim 14.

16. A process for recombinantly producing a polypeptide comprising culturing the host cell of claim 15 under conditions in which the polypeptide is expressed.

30

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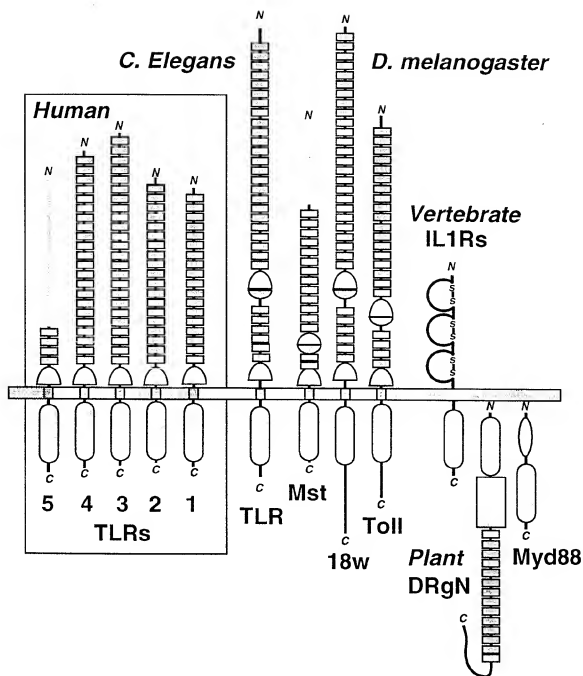
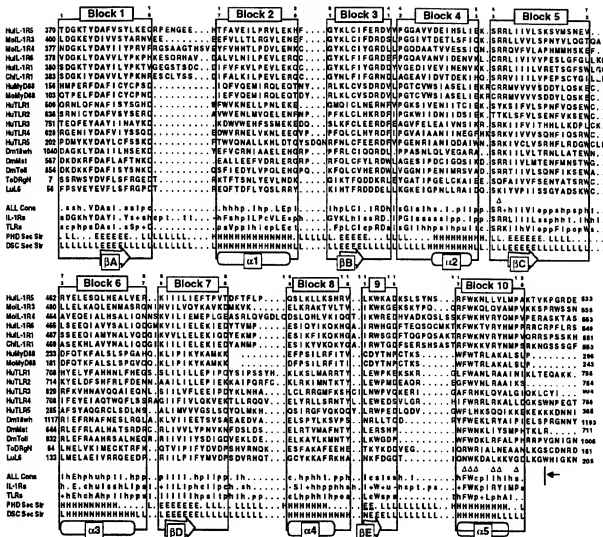
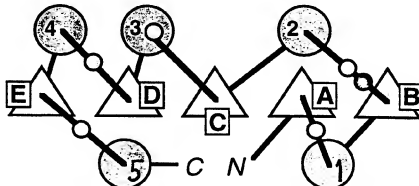


FIG. 1

**FIG. 2A**



**FIG. 2B**





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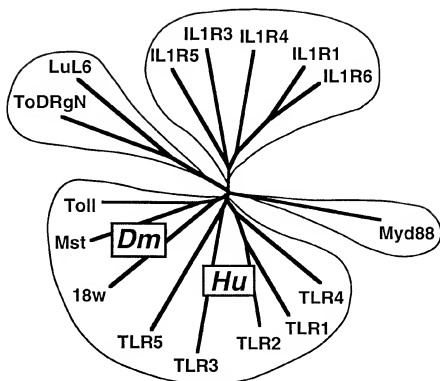


FIG. 3

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FIG. 4A



FIG. 4B

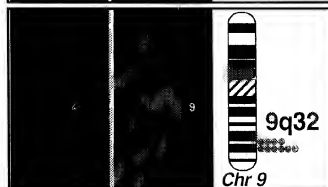


FIG. 4C



FIG. 4D

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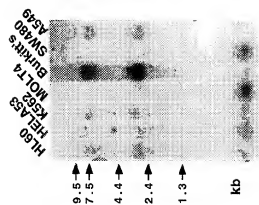


FIG. 5C

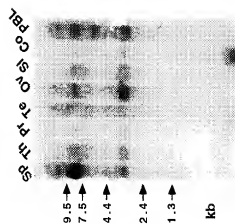


FIG. 5B

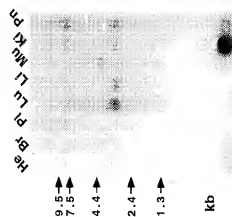


FIG. 5A

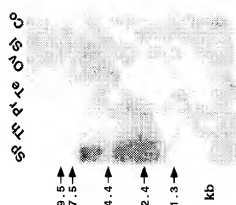


FIG. 5F

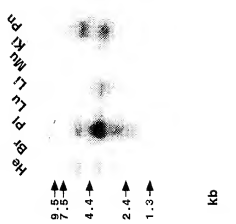


FIG. 5E



FIG. 5D